

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 16, 2004, 13:45:21 : Search time 739 Seconds

(without alignments)
10279.306 Million cell updates/sec

Title: US-10-063-735-127

Perfect score: 1505

Sequence: 1 cgggacgcgacccaagcag.....tcgcaaccccccaaaaaa 1505

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3327077 seqs, 2523723180 residues

Word size : 10

Total number of hits satisfying chosen parameters: 3143743

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1505	100.0	1505	US-10-206-915-377	Sequence 377, App
2	1505	100.0	1505	US-10-199-670-377	Sequence 377, App
3	1505	100.0	1505	US-10-201-858-377	Sequence 377, App
4	1505	100.0	1505	US-10-205-890-377	Sequence 377, App
5	1505	100.0	1505	US-10-208-024-377	Sequence 377, App
6	1505	100.0	1505	US-10-201-853-377	Sequence 377, App
7	1505	100.0	1505	US-10-063-745-127	Sequence 127, App
8	1505	100.0	1505	US-10-063-512-127	Sequence 127, App
9	1505	100.0	1505	US-10-063-513-127	Sequence 127, App
10	1505	100.0	1505	US-10-063-569-127	Sequence 127, App
11	1505	100.0	1505	US-10-063-551-127	Sequence 127, App
12	1505	100.0	1505	US-10-174-581-377	Sequence 377, App
13	1505	100.0	1505	US-10-176-483-377	Sequence 377, App
14	1505	100.0	1505	US-10-176-749-377	Sequence 377, App

15	1505	100.0	1505	13	US-10-176-914-377	Sequence 377, App
16	1505	100.0	1505	13	US-10-176-915-377	Sequence 377, App
17	1505	100.0	1505	13	US-10-063-555-127	Sequence 127, App
18	1505	100.0	1505	13	US-10-063-563-127	Sequence 127, App
19	1505	100.0	1505	13	US-10-063-594-127	Sequence 127, App
20	1505	100.0	1505	13	US-10-063-553-127	Sequence 127, App
21	1505	100.0	1505	13	US-10-063-554-127	Sequence 127, App
22	1505	100.0	1505	13	US-10-176-484-377	Sequence 377, App
23	1505	100.0	1505	13	US-10-180-550-377	Sequence 377, App
24	1505	100.0	1505	13	US-10-183-014-377	Sequence 377, App
25	1505	100.0	1505	13	US-10-187-738-377	Sequence 377, App
26	1505	100.0	1505	13	US-10-187-740-377	Sequence 377, App
27	1505	100.0	1505	13	US-10-187-883-377	Sequence 377, App
28	1505	100.0	1505	13	US-10-194-363-377	Sequence 377, App
29	1505	100.0	1505	13	US-10-194-460-377	Sequence 377, App
30	1505	100.0	1505	13	US-10-194-463-377	Sequence 377, App
31	1505	100.0	1505	13	US-10-194-484-377	Sequence 377, App
32	1505	100.0	1505	13	US-10-195-884-377	Sequence 377, App
33	1505	100.0	1505	13	US-10-195-896-377	Sequence 377, App
34	1505	100.0	1505	13	US-10-196-744-377	Sequence 377, App
35	1505	100.0	1505	13	US-10-196-755-377	Sequence 377, App
36	1505	100.0	1505	13	US-10-196-757-377	Sequence 377, App
37	1505	100.0	1505	13	US-10-197-704-377	Sequence 377, App
38	1505	100.0	1505	13	US-10-197-710-377	Sequence 377, App
39	1505	100.0	1505	13	US-10-198-758-377	Sequence 377, App
40	1505	100.0	1505	13	US-10-198-766-377	Sequence 377, App
41	1505	100.0	1505	13	US-10-199-304-377	Sequence 377, App
42	1505	100.0	1505	13	US-10-199-309-377	Sequence 377, App
43	1505	100.0	1505	13	US-10-199-313-377	Sequence 377, App
44	1505	100.0	1505	13	US-10-199-456-377	Sequence 377, App
45	1505	100.0	1505	13	US-10-201-329-377	Sequence 377, App

ALIGNMENTS

RESULT 1
US-10-206-915-377
; Sequence 377, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C513
; CURRENT APPLICATION NUMBER: US/10/206,915
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28

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; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-206-915-377

Query Match      100.0%; Score 1505; DB 13; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGATCGGACCAAGCAGGTCCGGCGCGCGCAGGAGAGCGCGGGCGTCAGCTCC 60
DB 1 CGCGGATCGGACCAAGCAGGTCCGGCGCGCGCAGGAGAGCGCGGGCGTCAGCTCC 60
QY 61 TCGACCCCGGTGTCGGGCTAGTCCAGCGAGCGGAGCGGCGGCGTGGGCCCATGGCCAGG 120
DB 61 TCGACCCCGGTGTCGGGCTAGTCCAGCGAGCGGAGCGGCGGCGTGGGCCCATGGCCAGG 120
QY 121 CCCGGATGAGCGGTGGCGGCGACCGGTGCGCGTGGTGGAGCGGGGCTCGGGGGGCATC 180
DB 121 CCCGGATGAGCGGTGGCGGCGACCGGTGCGCGTGGTGGAGCGGGGCGTGGGGGGGCATC 180
QY 181 GCGCGGCGGTGGCGGCGGCGGCTGGTCCAGCAGGAGCTGAAGGTGGTGGGCTGGCGCGCG 240
DB 181 GCGCGGCGGTGGCGGCGGCGGCTGGTCCAGCAGGAGCTGAAGGTGGTGGGCTGGCGCGCG 240
QY 241 ACTGTGGCAACATCGAGGAGCTGGCTGCTGAATGTGAAGTGAAGTGAAGTGAAGTGAAGT 300
DB 241 ACTGTGGCAACATCGAGGAGCTGGCTGCTGAATGTGAAGTGAAGTGAAGTGAAGTGAAGT 300
QY 301 TTGATCCCTACAGATGACCTATCAATGAAGAGGACATCCTCCATGTTCTCAGCT 360
DB 301 TTGATCCCTACAGATGACCTATCAATGAAGAGGACATCCTCCATGTTCTCAGCT 360
QY 361 ATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACATGCTGGCTGGCGCGGCGCT 420
DB 361 ATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACATGCTGGCTGGCGCGGCGCT 420
QY 421 GACACCTGCTCTCAGGAGCAGCAGTGGTGAAGAGGACATGTTCAATGTGAACGTGCTG 480
DB 421 GACACCTGCTCTCAGGAGCAGCAGTGGTGAAGAGGACATGTTCAATGTGAACGTGCTG 480
QY 481 GCGCTCAGCATCTGCACAGGAGGAGCCTACAGTCCATGAAGGAGCGGAATGTGAGCAT 540
DB 481 GCGCTCAGCATCTGCACAGGAGGAGCCTACAGTCCATGAAGGAGCGGAATGTGAGCAT 540
QY 541 GGGCACATCAATTAACATCAATAGCATGCTGGCCACCGAGTGTACCCCTGCTGTGACC 600
DB 541 GGGCACATCAATTAACATCAATAGCATGCTGGCCACCGAGTGTACCCCTGCTGTGACC 600
QY 601 CACTTCTATAGTCCACCAAGATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 601 CACTTCTATAGTCCACCAAGATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 CTTCCGGAGGCGCCAGACCCACATCCGAGCAGTGCATCTCTCCAGGTGTGGTGGAGACA 720
DB 661 CTTCCGGAGGCGCCAGACCCACATCCGAGCAGTGCATCTCTCCAGGTGTGGTGGAGACA 720
QY 721 CAATTCGCGCTTCAAACTCCACGACAGGACCCCTGAGAGGAGCTGCCACCTATGAGCAA 780
DB 721 CAATTCGCGCTTCAAACTCCACGACAGGACCCCTGAGAGGAGCTGCCACCTATGAGCAA 780
QY 781 ATGAAGTGTCTCAAAACCGGAGATGTGGCGGAGGCTGTATCTAGCTCTCAGCACCCCC 840
DB 781 ATGAAGTGTCTCAAAACCGGAGATGTGGCGGAGGCTGTATCTAGCTCTCAGCACCCCC 840
QY 841 GCACACATCCAGATTGGAGACATCCAGATGAGGCCCGCAGGAGGAGTGAACCTTAGTGA 900

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DB 841 GCACACATCCAGATTGGAGACATCCAGATGAGGCCCGCAGGAGGAGTGAACCTAGTGA 900
QY 901 TGGGAGCTCCTCCTTCCCTCCCGCAGCCCTTCATGCTTGCCTCCTGCTGCTGCTGCTGCTG 960
DB 901 TGGGAGCTCCTCCTTCCCTCCCGCAGCCCTTCATGCTTGCCTCCTGCTGCTGCTGCTGCTG 960
QY 961 TGTGATTCTCGGATCAGGGATACCACTTCTCCTGTCACACCCCGCAGGCGGCTAGAAA 1020
DB 961 TGTGATTCTCGGATCAGGGATACCACTTCTCCTGTCACACCCCGCAGGCGGCTAGAAA 1020
QY 1021 ATTGTTTGGATTTTATATATCATCTTGTCAAAATGCTTCAGTTGTAAATGTGAAAAATG 1080
DB 1021 ATTGTTTGGATTTTATATATCATCTTGTCAAAATGCTTCAGTTGTAAATGTGAAAAATG 1080
QY 1081 GGCCTGGGAAAGGAGGTGGTGTCCCTAAATGTTTAACTTGTAACTTGTTCCTGCTGCTG 1140
DB 1081 GGCCTGGGAAAGGAGGTGGTGTCCCTAAATGTTTAACTTGTAACTTGTTCCTGCTGCTG 1140
QY 1141 TGGGCACTTGGCCTTGTCTGCTCAGTGTCTTCCCTTTCACATGGGAAAGGAGTTGTG 1200
DB 1141 TGGGCACTTGGCCTTGTCTGCTCAGTGTCTTCCCTTTCACATGGGAAAGGAGTTGTG 1200
QY 1201 GCCAAAATCCCATCTTCTTTCACCTCAAGCTCTGCTGCTCAGGCTGGGCTGGCAGAGG 1260
DB 1201 GCCAAAATCCCATCTTCTTTCACCTCAAGCTCTGCTGCTCAGGCTGGGCTGGCAGAGG 1260
QY 1261 GAGCCTTTCACCTTATATCTGTTGTTATCCAGGGCTCCAGACTTCTCCTCTGCTGCTG 1320
DB 1261 GAGCCTTTCACCTTATATCTGTTGTTATCCAGGGCTCCAGACTTCTCCTCTGCTGCTG 1320
QY 1321 CCAGTGCACCTCTCCCGCTTATCTATCTCTGCTTCCGCTCCCGCAGCCAGTCTTGGCT 1380
DB 1321 CCAGTGCACCTCTCCCGCTTATCTATCTCTGCTTCCGCTCCCGCAGCCAGTCTTGGCT 1380
QY 1381 TCTTGTCCCTCTCGGGGTCACTCCCTCACTCTGACTCTGACTATGGCAGCAGAACCA 1440
DB 1381 TCTTGTCCCTCTCGGGGTCACTCCCTCACTCTGACTCTGACTATGGCAGCAGAACCA 1440
QY 1441 GGGCCTGGCCAGTGGATTTTCATGCTGATCAATTAATAAGAAATGCAACCAAAAAA 1500
DB 1441 GGGCCTGGCCAGTGGATTTTCATGCTGATCAATTAATAAGAAATGCAACCAAAAAA 1500
QY 1501 AAAAA 1505
DB 1501 AAAAA 1505

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RESULT 2
US-10-199-670-377
; Sequence 377, Application US/10199670
; Publication No. US20040033560A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C401
; CURRENT APPLICATION NUMBER: US/10199, 670
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18

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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C464
; CURRENT APPLICATION NUMBER: US/10/201,858
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
; ORGANISM: Homo
US-10-201-858-377

Query Match      100.0%; Score 1505; DB 13; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CGCGGATCGGACCCCAAGCAGGTGCGCGCGCGCGGCGGAGAGCGCGCGGCGGTGAGTCTCC 60
Db      1  CGCGGATCGGACCCCAAGCAGGTGCGCGCGCGCGGCGGAGAGCGCGCGGCGGTGAGTCTCC 60

Qy      61  TCGACCCCGCGTGTGGGCTAGTCTCAGCAGGCGGAGCGGCGGCGGTGAGGCGGCGGCGGCGG 120
Db      61  TCGACCCCGCGTGTGGGCTAGTCTCAGCAGGCGGAGCGGCGGCGGTGAGGCGGCGGCGGCGG 120

Qy      121  CCGGCGATGGAGCGGTGGCGGACCGGCTGGGCTGGTGACGGGCGGCTCGGGGGGCGATC 180
Db      121  CCGGCGATGGAGCGGTGGCGGACCGGCTGGGCTGGTGACGGGCGGCTCGGGGGGCGATC 180

Qy      181  GCGCGGCGGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db      181  GCGCGGCGGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240

Qy      241  ACTGTGGCAACATCGAGGAGTGGCTGCTGAATGTAAGTGCAGGTCAGGTCACCGGAGCT 300
Db      241  ACTGTGGCAACATCGAGGAGTGGCTGCTGAAATGTAAGTGCAGGTCACCGGAGCT 300

Qy      301  TTGATCCCGCTACAGATGTGACCTATCAAAATGAAGAGGACATCCCTCTCCATGTCTCAGCT 360
Db      301  TTGATCCCGCTACAGATGTGACCTATCAAAATGAAGAGGACATCCCTCTCCATGTCTCAGCT 360

Qy      361  ATCCGTTCTCAGCAGCGGCTGTAGACATCTGCATCAACAATGTGCTGGCTTGGCGCGGCGCT 420
Db      361  ATCCGTTCTCAGCAGCGGCTGTAGACATCTGCATCAACAATGTGCTGGCTTGGCGCGGCGCT 420

Qy      421  GACACCCCTGCTCAGGCGAGCAGCAGTGGTGGAGAGGACATGTTCAATGTCAAGTGTCTG 480
Db      421  GACACCCCTGCTCAGGCGAGCAGCAGTGGTGGAGAGGACATGTTCAATGTCAAGTGTCTG 480

Qy      481  GCCCTCAGCATCTGCACACGGGAAGCCTACCAAGTCCATGAAGAGCGGAATGTGGACCGAT 540
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RESULT 4

Db 1201 GCCAAATCCCATCTTCTTGACCTCAACGCTGTGGCTCAGGGCTGGGGTGGCAGAGG 1260
 Qy 1261 GAGGCTTACCTTATATCTGTGTGTATATCCAGGGCTCCAGACTTCTCTCTGCTGC 1320
 Db 1261 GAGGCTTACCTTATATCTGTGTGTATATCCAGGGCTCCAGACTTCTCTCTGCTGC 1320
 Qy 1321 CCCACTGCACCTCTGCCCTTATCTATCTCTTCTGGCTCCCGAGCCAGCTCTGGCT 1380
 Db 1321 CCCACTGCACCTCTGCCCTTATCTATCTCTTCTGGCTCCCGAGCCAGCTCTGGCT 1380
 Qy 1381 TCTTGTCCCTCTCCGGGTATCTCCCTCCACTCTGACTCTGACTATGGCAGCAGAACCA 1440
 Db 1381 TCTTGTCCCTCTCCGGGTATCTCCCTCCACTCTGACTCTGACTATGGCAGCAGAACCA 1440
 Qy 1441 GGGCTGCGCCAGTGGATTCATGGTGATCATTTAAAGAAAAATGCAACCAAAAAA 1500
 Db 1441 GGGCTGCGCCAGTGGATTCATGGTGATCATTTAAAGAAAAATGCAACCAAAAAA 1500
 Qy 1501 AAAAA 1505
 Db 1501 AAAAA 1505

RESULT 6

US-10-201-853-377
 ; Sequence 377, Application US/10201853
 ; Publication No. US20040053358A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C465
 ; CURRENT APPLICATION NUMBER: US/10/201,853
 ; CURRENT FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: 10/052586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 377
 ; LENGTH: 1505
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-201-853-377

Query Match

100.0%; Score 1505; DB 13; Length 1505;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CGCGATCGAACCCCAAGCAGGTGCGCGCGCGCGCGAGAGCGCGCGCGGTCTCAGTCC 60
 Db 1 CGCGATCGAACCCCAAGCAGGTGCGCGCGCGCGCGAGAGCGCGCGCGGTCTCAGTCC 60
 Qy 61 TCGACCCCGGTGTGGGCTAGTCCAGCGAGCGCGAGCGCGCGCGGTGGGCGGCGGCGG 120
 Db 61 TCGACCCCGGTGTGGGCTAGTCCAGCGAGCGCGAGCGCGCGCGGTGGGCGGCGGCGG 120
 Qy 121 CCGGCATGAGCGGTGCGCGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCG 180
 Db 121 CCGGCATGAGCGGTGCGCGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCG 180
 Qy 181 GCGCGCGCGGTGCGCGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGCG 240
 Db 181 GCGCGCGCGGTGCGCGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGCG 240
 Qy 241 ACTGTGGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGTGCAGGCTACCCCGGACT 300
 Db 241 ACTGTGGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGTGCAGGCTACCCCGGACT 300
 Qy 301 TTGATCCCTACAGATGTGACCTATCAATGAAGCAGACATCCCTCTCCATGTTCTCAGCT 360
 Db 301 TTGATCCCTACAGATGTGACCTATCAATGAAGCAGACATCCCTCTCCATGTTCTCAGCT 360
 Qy 361 ATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTGGCGCGGCT 420
 Db 361 ATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTGGCGCGGCT 420
 Qy 421 GACACCTCTCTCAGGAGCAGCGGTGTTGAGGAGACATGTTCAATGTGAAGTGGT 480
 Db 421 GACACCTCTCTCAGGAGCAGCGGTGTTGAGGAGACATGTTCAATGTGAAGTGGT 480
 Qy 481 GCCCTCAGCATCTGCACACGGGAAGCCTACCACTCCATGAAGGAGCGGAATGTGGACAT 540
 Db 481 GCCCTCAGCATCTGCACACGGGAAGCCTACCACTCCATGAAGGAGCGGAATGTGGACAT 540
 Qy 541 GGGCACATCAATTAACATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACC 600
 Db 541 GGGCACATCAATTAACATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACC 600
 Qy 601 CACTTCTATAGTGCACCAAGTATGCGCTCACTGCGCTGACAGGAGCTGAGGCAAGAG 660
 Db 601 CACTTCTATAGTGCACCAAGTATGCGCTCACTGCGCTGACAGGAGCTGAGGCAAGAG 660
 Qy 661 CTTGGGAGGCGCCAGAGCCACATCCGAGCCACGTCATCTCTCCAGTGTGGTGGAGACA 720
 Db 661 CTTGGGAGGCGCCAGAGCCACATCCGAGCCACGTCATCTCTCCAGTGTGGTGGAGACA 720
 Qy 721 CAATTGCGCTTCAAACTCCACGACCAAGGACCTTGAGAGGAGCTGCCACTATGAGCAA 780
 Db 721 CAATTGCGCTTCAAACTCCACGACCAAGGACCTTGAGAGGAGCTGCCACTATGAGCAA 780
 Qy 781 ATGAAGTGTCTCAAAACCGGAGGATGTGGCGAGGCTGTTATCTACGCTCTCAGCACCC 840
 Db 781 ATGAAGTGTCTCAAAACCGGAGGATGTGGCGAGGCTGTTATCTACGCTCTCAGCACCC 840
 Qy 841 GCACACATCCAGATTGGAGACATCCAGATGAGGCGCCACGAGAGGTGACCTAGTACTG 900
 Db 841 GCACACATCCAGATTGGAGACATCCAGATGAGGCGCCACGAGAGGTGACCTAGTACTG 900
 Qy 901 TGGGAGCTCTCTCTCCCTCCCAACCTTCATGCGCTTGGCTCTCTCTCTCTCTCTCT 960
 Db 901 TGGGAGCTCTCTCTCTCCCTCCCAACCTTCATGCGCTTGGCTCTCTCTCTCTCTCTCT 960
 Qy 961 TGTGATTCTTGGATCAGGGATACCACTTCTCTGTCACACCCCGAGCGGCTAGAAA 1020
 Db 961 TGTGATTCTTGGATCAGGGATACCACTTCTCTGTCACACCCCGAGCGGCTAGAAA 1020
 Qy 1021 ATTGTTTGGATTCTTATATCATCTTGTCAAAATGCTTCAATGTAATGTGAAAATG 1080

Db 1021 ATTTGTTTGAGATTTTATATCATCTTGTCAAATGCTTCACTTGTAAATGTGAAAATG 1080
Qy 1081 GGCTGGGAAAGAGGTGGTCCCTAATGTTTACTTGTAACTTGTCTTGTGCCCC 1140
Db 1081 GGCTGGGAAAGAGGTGGTCCCTAATGTTTACTTGTAACTTGTCTTGTGCCCC 1140
Qy 1141 TGGGCACCTTGGCTTTGCTGCTCTCACTGCTCTTCCCTTTGACATGGGAAAGGAGTTGTG 1200
Db 1141 TGGGCACCTTGGCTTTGCTGCTCTCACTGCTCTTCCCTTTGACATGGGAAAGGAGTTGTG 1200
Qy 1201 GCCAAATCCCAATCTTCTTGACCTCAACGCTCTGTGGCTCAGGGCTGGGGTGGCAGAGG 1260
Db 1201 GCCAAATCCCAATCTTCTTGACCTCAACGCTCTGTGGCTCAGGGCTGGGGTGGCAGAGG 1260
Qy 1261 GAGGCTTCACCTTATATCTGTTGTTATCCAGGCTCCAGACTTCCCTCTGCTGCTGC 1320
Db 1261 GAGGCTTCACCTTATATCTGTTGTTATCCAGGCTCCAGACTTCCCTCTGCTGCTGC 1320
Qy 1321 CCCACTGACCTCTCCCTCTTATCTATCTCTCTGCTCCCGAGCCAGCTTGGCT 1380
Db 1321 CCCACTGACCTCTCCCTCTTATCTATCTCTCTGCTCCCGAGCCAGCTTGGCT 1380
Qy 1381 TCTTGTCCCTCTCGGGTCACTCCCTCCACTCTGACTCTGACTATGGCAGCAGAACCA 1440
Db 1381 TCTTGTCCCTCTCGGGTCACTCCCTCCACTCTGACTCTGACTATGGCAGCAGAACCA 1440
Qy 1441 GGGCTGGCCAGTGGATTTATGGTGATCATTAATAAAGAAAAATCCAAACCAAAAAA 1500
Db 1441 GGGCTGGCCAGTGGATTTATGGTGATCATTAATAAAGAAAAATCCAAACCAAAAAA 1500
Qy 1501 AAAAA 1505
Db 1501 AAAAA 1505

RESULT 7

US-10-063-745-127

; Sequence 127, Application US/10063745

; Publication No. US20040058411A1

; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3230R1C1

; CURRENT APPLICATION NUMBER: US/10/063,745

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 170

; SEQ ID NO 127

; LENGTH: 1505

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-063-745-127

Query Match 100.0%; Score 1505; DB 13; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGGATCGGACCAAGCAGGTCCGGCGCGGCGGAGAGCGCGCGGGGCTCAGCTCC 60

Db 1 CGCGGATCGGACCAAGCAGGTCCGGCGCGGCGGAGAGCGCGCGGGGCTCAGCTCC 60

Qy 61 TCGACCCCGGTGTCGGGCTAGTCCAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120

Db 61 TCGACCCCGGTGTCGGGCTAGTCCAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120

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QY 1201 GCCAAATCCCATCTTCTTGACCTCAACGCTCTGTGGCTCAGGGCTGGGTGGCAGG 1260
Db |||||
QY 1201 GCCAAATCCCATCTTCTTGACCTCAACGCTCTGTGGCTCAGGGCTGGGTGGCAGG 1260
Db |||||
QY 1261 GAGGCTTCCATCTATATCTGTGTGTTATCCAGGGCTCCAGACTTCTCTCTGCTGTC 1320
Db |||||
QY 1261 GAGGCTTCCATCTATATCTGTGTGTTATCCAGGGCTCCAGACTTCTCTCTGCTGTC 1320
Db |||||
QY 1321 CCAGTGCACCTCTCCCTCTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
Db |||||
QY 1381 TCTGTCCCTCTCTGGGCTATCCCTCCACTCTGACTCTGACTATGCGAGCAGAACCA 1440
Db |||||
QY 1381 TCTGTCCCTCTCTGGGCTATCCCTCCACTCTGACTCTGACTATGCGAGCAGAACCA 1440
Db |||||
QY 1441 GGGCTGGCCAGTGGATTTTCATGGTGATCATTTAAAAAGAAAAATCGCAACCAAAAA 1500
Db |||||
QY 1501 AAAAA 1505
Db |||||
QY 1501 AAAAA 1505
Db |||||

RESULT 8
US-10-063-512-127
; Sequence 127, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/063,512
; PRIORITY FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 127
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-512-127

Query Match 100.0%; Score 1505; DB 13; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGATCGGACCCAGCAGGTCCGCGCGCGGCGGAGAGCGGCGGCGTCACTCC 60
Db 1 CGCGATCGGACCCAGCAGGTCCGCGCGCGGCGGAGAGCGGCGGCGTCACTCC 60

QY 61 TCGACCCCGGTGTGGGCTAGTTCAGAGCGAGCGGCGGCGGCGGCGGCGGCGGCGG 120
Db 61 TCGACCCCGGTGTGGGCTAGTTCAGAGCGAGCGGCGGCGGCGGCGGCGGCGGCGG 120

QY 121 CCGGATCGGAGCGGTGGCGGACCGGCTGGCGTGGTGAAGGGGCGCTCGGGGGGATC 180
Db 121 CCGGATCGGAGCGGTGGCGGACCGGCTGGCGTGGTGAAGGGGCGCTCGGGGGGATC 180

QY 181 GCGCGGCGGTGGCGGCGGCGGCTGGTCCAGAGGAGCTGAAGGTGGGCTGGCGGCGG 240
Db 181 GCGCGGCGGTGGCGGCGGCGGCTGGTCCAGAGGAGCTGAAGGTGGGCTGGCGGCGG 240

QY 241 ACTGTGGGCAACATCGAGGAGTGGCTGCTGTAATGTAAGAGTGCAGGCTACCCCGGACT 300

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Db 241 ACTGTGGGCAACATCGAGGAGTGGCTGCTGTAATGTAAGAGTGCAGGCTACCCGGGACT 300
QY 301 TTGATCCCTTACAGATGTGACCTATCAAAATGAAGAGACATCTCTCTCAATGTTCTAGCT 360
Db 301 TTGATCCCTTACAGATGTGACCTATCAAAATGAAGAGACATCTCTCTCAATGTTCTAGCT 360
QY 361 ATCGTTCTCAGACAGCGGTGTAGACATCTGATCAACATGCTGCTGCTGGCTGGCGGCT 420
Db 361 ATCGTTCTCAGACAGCGGTGTAGACATCTGATCAACATGCTGCTGCTGGCTGGCGGCT 420
QY 421 GACACCTCTGCTCTCAGGAGCAGCAGGTGGTTGGAAGGACATGTTCAATGTGAACGTGTG 480
Db 421 GACACCTCTGCTCTCAGGAGCAGCAGGTGGTTGGAAGGACATGTTCAATGTGAACGTGTG 480
QY 481 GCCCTCAGATCTGCAACCGGAAGCTTACAGTCCATGAAGAGCGGAATGTGAGCAT 540
Db 481 GCCCTCAGATCTGCAACCGGAAGCTTACAGTCCATGAAGAGCGGAATGTGAGCAT 540
QY 541 GGGCAGCATATTAACTCAATAGCATCTGCGCACCGAGTGTACCCCTGCTGTGAC 600
Db 541 GGGCAGCATATTAACTCAATAGCATCTGCGCACCGAGTGTACCCCTGCTGTGAC 600
QY 601 CACTTCTATAGTGCACCAAGTATGCGCTCACTGCGCTGACAGAGGACTGAGCAAGAG 660
Db 601 CACTTCTATAGTGCACCAAGTATGCGCTCACTGCGCTGACAGAGGACTGAGCAAGAG 660
QY 661 CTTGGAGGCGGAGCCACATCCAGGACACGTCGATCTCTCAGGTGTGGTGAGACA 720
Db 661 CTTGGAGGCGGAGCCACATCCAGGACACGTCGATCTCTCAGGTGTGGTGAGACA 720
QY 721 CAATTGCGCTTCAAACTCCAGCAAGGACCTGAGAGGAGCTGCCACCTATGAGCAA 780
Db 721 CAATTGCGCTTCAAACTCCAGCAAGGACCTGAGAGGAGCTGCCACCTATGAGCAA 780
QY 781 ATGAAGTGTCTCAAAACCGAGGATGTGGCGAGGCTGTATCTACGCTCTCAGCACCC 840
Db 781 ATGAAGTGTCTCAAAACCGAGGATGTGGCGAGGCTGTATCTACGCTCTCAGCACCC 840
QY 841 GCACATCCAGATTTGAGACATCCAGATGAGGCGGCGGAGGAGTGAACCTAGTACTG 900
Db 841 GCACATCCAGATTTGAGACATCCAGATGAGGCGGCGGAGGAGTGAACCTAGTACTG 900
QY 901 TGGAGCTCTCTCTCCCTCCCACTCTCATGCTTCCCTCTCTCTCTCTCTCTCTCTCTCT 960
Db 901 TGGAGCTCTCTCTCTCCCTCCCACTCTCATGCTTCCCTCTCTCTCTCTCTCTCTCTCT 960
QY 961 TGTTGATTTCTGGATCACGGGATACCACTTCTCTGTCACACCCCGGAGCGGCTAGAAA 1020
Db 961 TGTTGATTTCTGGATCACGGGATACCACTTCTCTGTCACACCCCGGAGCGGCTAGAAA 1020
QY 1021 ATTTGTTGAGATTTTATATCATCTTGTGTAATGCTTCAAGTGTAAATGTGAAAAATG 1080
Db 1021 ATTTGTTGAGATTTTATATCATCTTGTGTAATGCTTCAAGTGTAAATGTGAAAAATG 1080
QY 1081 GGCTGGGGAAGGAGGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
Db 1081 GGCTGGGGAAGGAGGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
QY 1141 TGGGCACTTGGGCTTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
Db 1141 TGGGCACTTGGGCTTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
QY 1201 GCCAAATCCCATCTTCTTGACCTCAACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
Db 1201 GCCAAATCCCATCTTCTTGACCTCAACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY 1261 GAGGCTTCACTTATATCTGTGTGTTATCCAGGCTCCAGACTTCTCTCTCTGCTGCTG 1320
Db 1261 GAGGCTTCACTTATATCTGTGTGTTATCCAGGCTCCAGACTTCTCTCTCTGCTGCTG 1320
QY 1321 CCCACTGCACCTCTCCCTCTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380

```

Db 1321 CCCACTGCACCCCTCTCCGCCCTTATCTATCTCTCTCTCCGCCCTCCCGACCCAGCTTTGGCT 1380
Qy 1381 TCTTCTCCCTCTCTCCGCCCTATCCCTCCACTCTGACTCTGACTATGGGACGAGAACCA 1440
Db 1381 TCTTCTCCCTCTCTCCGCCCTATCCCTCCACTCTGACTCTGACTATGGGACGAGAACCA 1440
Qy 1441 GGGCTCGGCCAGTGTGATTTATGTTGATCATTAATAAAGAAAAATCGAACCAAAAAA 1500
Db 1441 GGGCTCGGCCAGTGTGATTTATGTTGATCATTAATAAAGAAAAATCGAACCAAAAAA 1500
Qy 1501 AAAAA 1505
Db 1501 AAAAA 1505

RESULT 9

US-10-063-513-127
; Sequence 127, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; PENDING FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 127
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-513-127

Query Match 100.0%; Score 1505; DB 13; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGCGGATCGGACCCAGCAGGTGCGCGCGCGCGGAGAGAGCGCGCGCGTCCAGTCC 60
Db 1 CGCGGATCGGACCCAGCAGGTGCGCGCGCGGAGAGAGCGCGCGCGTCCAGTCC 60
Qy 61 TCGACCCCGGTGTGCGGCTAGTCCAGCGAGCGCGCGCGCGTGGGCCCATGCCAGG 120
Db 61 TCGACCCCGGTGTGCGGCTAGTCCAGCGAGCGCGCGCGCGTGGGCCCATGCCAGG 120
Qy 121 CCGGCGATGAGCGGTGCGCGCGAGCGCGTGGCTGGTACGCGGCGCTCGGGGGGCGATC 180
Db 121 CCGGCGATGAGCGGTGCGCGCGAGCGCGTGGCTGGTACGCGGCGCTCGGGGGGCGATC 180
Qy 181 GCGCGGCGGTGCGCGCGCGCGCGTGGTCCAGCGAGCGTGAAGGTGGTGGGTGCGCGCGC 240
Db 181 GCGCGGCGGTGCGCGCGCGCGCGTGGTCCAGCGAGCGTGAAGGTGGTGGGTGCGCGCGC 240
Qy 241 ACTGTGGGCAACATCGAGGAGTGGCTGCTGAATGTGAAGTGCAGGCTACCCCGGACT 300
Db 241 ACTGTGGGCAACATCGAGGAGTGGCTGCTGAATGTGAAGTGCAGGCTACCCCGGACT 300
Qy 301 TTGATCCCTTACAGATGACCTATCAATGAAGAGGACATCCCTCTCAATGTTCTCAGCT 360
Db 301 TTGATCCCTTACAGATGACCTATCAATGAAGAGGACATCCCTCTCAATGTTCTCAGCT 360
Qy 361 ATCCGTTCTCAGCACAGCGGTGACATCTGCATCAACATGCTGGCTTGGCCCGCGCT 420
Db 361 ATCCGTTCTCAGCACAGCGGTGACATCTGCATCAACATGCTGGCTTGGCCCGCGCT 420

Qy 421 GACACCCCTGCTCTCAGGCGAGCACAGTGGTGGAAAGGACATGTTCAATGTGAACGTGCTG 480
Db 421 GACACCCCTGCTCTCAGGCGAGCACAGTGGTGGAAAGGACATGTTCAATGTGAACGTGCTG 480
Qy 481 GCCCTCAGCATCTGCACACGGGAGGCTTACAGTCCATGAAGGAGGGAATGTGACCAT 540
Db 481 GCCCTCAGCATCTGCACACGGGAGGCTTACAGTCCATGAAGGAGGGAATGTGACCAT 540
Qy 541 GGGCACATCAATTAACATCAATAGCATGCTGGCCACCGAGTGTACCCCTGCTCTGACC 600
Db 541 GGGCACATCAATTAACATCAATAGCATGCTGGCCACCGAGTGTACCCCTGCTCTGACC 600
Qy 601 CACTTCTATAGTGCACCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 CACTTCTATAGTGCACCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy 661 CTTGGGAGGCGCCAGACCCACATCCGAGCCAGTGCATCTCTCCAGGTGTGGTGAGACA 720
Db 661 CTTGGGAGGCGCCAGACCCACATCCGAGCCAGTGCATCTCTCCAGGTGTGGTGAGACA 720
Qy 721 CAATTGCGCTTCAAACTCCACGACAAAGGACCTTGAGAAAGGAGCTGCCACCTATGAGCAA 780
Db 721 CAATTGCGCTTCAAACTCCACGACAAAGGACCTTGAGAAAGGAGCTGCCACCTATGAGCAA 780
Qy 781 ATGAAGTGTCTCAAACTCCACGAGGATGTCGCGAGGCTGTATCTAGTCTCTCAGCACCC 840
Db 781 ATGAAGTGTCTCAAACTCCACGAGGATGTCGCGAGGCTGTATCTAGTCTCTCAGCACCC 840
Qy 841 GCACATCTCAGATTGGAGACATCCAGATGAGGCCACGAGGAGCTGACCTAGTACTG 900
Db 841 GCACATCTCAGATTGGAGACATCCAGATGAGGCCACGAGGAGCTGACCTAGTACTG 900
Qy 901 TGGAGCT 960
Db 901 TGGAGCT 960
Qy 961 TGTGATTTCTGGATCAGGATACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
Db 961 TGTGATTTCTGGATCAGGATACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
Qy 1021 ATTTGTTTGAGATTTTAT 1080
Db 1021 ATTTGTTTGAGATTTTAT 1080
Qy 1081 GGCTGGGAAAGGAGGTGGTGCCTAATGTTTAACTTTTAACTTTTAACTTTTAACTTTT 1140
Db 1081 GGCTGGGAAAGGAGGTGGTGCCTAATGTTTAACTTTTAACTTTTAACTTTTAACTTTT 1140
Qy 1141 TGGGCACTTGGCTTCT 1200
Db 1141 TGGGCACTTGGCTTCT 1200
Qy 1201 GCCAAAAATCCCACTCTTCTGACCTCAAGCTCTGCTGCTCAGGCTCAGGCTGGGCTG 1260
Db 1201 GCCAAAAATCCCACTCTTCTGACCTCAAGCTCTGCTGCTCAGGCTGGGCTGGCAGAG 1260
Qy 1261 GAGGCTTACCTTAT 1320
Db 1261 GAGGCTTACCTTAT 1320
Qy 1321 CCACCTGACCT 1380
Db 1321 CCACCTGACCT 1380
Qy 1381 TCTTGTCT 1440
Db 1381 TCTTGTCT 1440
Qy 1441 GGGCTGGCCCGAGTGGATTTATGTTGATCATTAATAAAGAAAAATCGAACCAAAAAA 1500
Db 1441 GGGCTGGCCCGAGTGGATTTATGTTGATCATTAATAAAGAAAAATCGAACCAAAAAA 1500

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QY 1501 AAAAA 1505
Db 1501 AAAAA 1505

RESULT 10
US-10-063-569-127
; Sequence 127, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 127
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-569-127

Query Match 100.0%; Score 1505; DB 13; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGATCGGACCAAGCAGTCCGCGCGCGCGCGAGAGCGCGCGCGTCCAGTCC 60
Db 1 CGCGATCGGACCAAGCAGTCCGCGCGCGCGCGAGAGCGCGCGCGTCCAGTCC 60

61 TCGACCCCGCGTGGGCTAGTCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
61 TCGACCCCGCGTGGGCTAGTCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 120

121 CCGCGCATGAGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
121 CCGCGCATGAGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

181 GCGCGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
181 GCGCGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240

241 ACTGTGGCAACATCGAGGAGTGGCTGCTGAAATGAAGAGTGCAGGCTACCCGCG 300
241 ACTGTGGCAACATCGAGGAGTGGCTGCTGAAATGAAGAGTGCAGGCTACCCGCG 300

301 TTGATCCCTCAGATGAGCCTATCAAAATGAAGAGGACATCTCTCCATGTTCTCAG 360
301 TTGATCCCTCAGATGAGCCTATCAAAATGAAGAGGACATCTCTCCATGTTCTCAG 360

361 ATCCGTTCTCAGCAGCGGTGAGACATCTGCATCAACATGCTGGGCTGGCGCGCG 420
361 ATCCGTTCTCAGCAGCGGTGAGACATCTGCATCAACATGCTGGGCTGGCGCGCG 420

421 GACACCCCTGCTCTCAGGCGAGCAGTGGTGGAGGACATGTTCAATGTGAACGTGCT 480
421 GACACCCCTGCTCTCAGGCGAGCAGTGGTGGAGGACATGTTCAATGTGAACGTGCT 480

481 GCCCTCAGCATCTGCACACGGGAAACCTACAGTCCATGAGGAGCGGAAATGAGCAG 540
481 GCCCTCAGCATCTGCACACGGGAAACCTACAGTCCATGAGGAGCGGAAATGAGCAG 540

541 GGGCACATCAATTAACATAGCATGTCTGCCACCGAGTGTACCCCTCTCTGTGACC 600

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RESULT 11
 US-10-063-127
 ; Sequence 127, Application US/10063551
 ; Publication No. US2002018349A1
 ; GENERAL INFORMATION:

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Db 541 GGGCACATCAATTAACATAGCATGTCTGCCACCGAGTGTACCCCTCTGTGACC 600
QY 601 CACTTCTATAGTCCCAAGATATGCGCTCACTGCGCTGACAGAGGACTGAGGCAAGAG 660
Db 601 CACTTCTATAGTCCCAAGATATGCGCTCACTGCGCTGACAGAGGACTGAGGCAAGAG 660
QY 661 CTTTGGGAGGCCAGAGCCACATCCGAGCCACGTCGATCTCTCAGGTGGTGGAGACA 720
Db 661 CTTTGGGAGGCCAGAGCCACATCCGAGCCACGTCGATCTCTCAGGTGGTGGAGACA 720
QY 721 CAATTCGCTTCAAACCTCCACGACAGGACCTGAGAAGGAGCTGCCACTATGAGCAA 780
Db 721 CAATTCGCTTCAAACCTCCACGACAGGACCTGAGAAGGAGCTGCCACTATGAGCAA 780
QY 781 ATGAAGTGTCTCAAAACCCGAGGATGTGGCGAGGCTGTTATCTACGTCCTCAGCACCC 840
Db 781 ATGAAGTGTCTCAAAACCCGAGGATGTGGCGAGGCTGTTATCTACGTCCTCAGCACCC 840
QY 841 GCACACATCCAGATTCGAGACATCCAGATGAGCCACGAGCAGGAGTACCTAGTACTG 900
Db 841 GCACACATCCAGATTCGAGACATCCAGATGAGCCACGAGCAGGAGTACCTAGTACTG 900
QY 901 TGGGAGCTCCTCCTTCCCTCCACACCTTCAATGGCTTGCCTCCTGCTCTGGATTTAGG 960
Db 901 TGGGAGCTCCTCCTTCCCTCCACACCTTCAATGGCTTGCCTCCTGCTCTGGATTTAGG 960
QY 961 TGTGATTTCTGGATACACGGGATACCACTTCTCTCCACACCCCGAGGCGGTAGAAA 1020
Db 961 TGTGATTTCTGGATACACGGGATACCACTTCTCTCCACACCCCGAGGCGGTAGAAA 1020
QY 1021 ATTTGTTTGGATTTTATATCATCTTGTCAAAATGCTTCAGTGTAAATGTGAAAAATG 1080
Db 1021 ATTTGTTTGGATTTTATATCATCTTGTCAAAATGCTTCAGTGTAAATGTGAAAAATG 1080
QY 1081 GGCTGGGGAAAGAGGTGGTGCCTAAATGTTTACTTGTAACTTGTCTTCTGCCCC 1140
Db 1081 GGCTGGGGAAAGAGGTGGTGCCTAAATGTTTACTTGTAACTTGTCTTCTGCCCC 1140
QY 1141 TGGSCATTTGGCTTTCTGCTCTCAGTGTCTTCCCTTTTGACATGGGAAAGAGTTGTG 1200
Db 1141 TGGSCATTTGGCTTTCTGCTCTCAGTGTCTTCCCTTTTGACATGGGAAAGAGTTGTG 1200
QY 1201 GCGAAATCCCATCTTTTGGACCTCAAGTGTGCTGCTGAGGCTGGGCTGGCAGAGG 1260
Db 1201 GCGAAATCCCATCTTTTGGACCTCAAGTGTGCTGCTGAGGCTGGGCTGGCAGAGG 1260
QY 1261 GAGGCTTTCACCTTATATCTGTGTGTTATCCAGGCTCCAGACTTCTCCTCTGCTGTC 1320
Db 1261 GAGGCTTTCACCTTATATCTGTGTGTTATCCAGGCTCCAGACTTCTCCTCTGCTGTC 1320
QY 1321 CCACTGACACCTCTCCCTCTTATCTATCTCCTTCTGGCTCCCGAGGCTTGGCT 1380
Db 1321 CCACTGACACCTCTCCCTCTTATCTATCTCCTTCTGGCTCCCGAGGCTTGGCT 1380
QY 1381 TCTTGTCCCTCTGGGCTCATCCCTCACTCTGACTGCTGACTGAGCAGAGCAACCA 1440
Db 1381 TCTTGTCCCTCTGGGCTCATCCCTCACTCTGACTGCTGACTGAGCAGAGCAACCA 1440
QY 1441 GGGGCTGGCCAGTGGATTTTCAATGGTATCAATTTAAAAAGAAAAATCGCAACCAAAAA 1500
Db 1441 GGGGCTGGCCAGTGGATTTTCAATGGTATCAATTTAAAAAGAAAAATCGCAACCAAAAA 1500
QY 1501 AAAAA 1505
Db 1501 AAAAA 1505

```


; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,551
 ; CURRENT FILING DATE: 2002-05-02
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 127
 ; LENGTH: 1505
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-063-551-127

Query Match 100.0%; Score 1505; DB 13; Length 1505;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CGCGCATCGGACCCCAAGCAGGTGCGGGCGGCGGAGAGCGCGGGGGGTGAGTCC	60
Db	1	CGCGCATCGGACCCCAAGCAGGTGCGGGCGGCGGAGAGCGCGGGGGGTGAGTCC	60
Qy	61	TCGACCCCGGTGTCGGGTAGTCCAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG	120
Db	61	TCGACCCCGGTGTCGGGTAGTCCAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG	120
Qy	121	CCGCGCATGAGCGGTGCGGCGGACCGGCTGCGGTGAGCGGGGCGCTCGGGGGGATC	180
Db	121	CCGCGCATGAGCGGTGCGGCGGACCGGCTGCGGTGAGCGGGGCGCTCGGGGGGATC	180
Qy	181	GGCGGGCGGTGGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	240
Db	181	GGCGGGCGGTGGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	240
Qy	241	ACTGTGGCAACATCGAGGAGTGGCTGCTGAAATGTAAGAGTGAGGCTACCCCGGACT	300
Db	241	ACTGTGGCAACATCGAGGAGTGGCTGCTGAAATGTAAGAGTGAGGCTACCCCGGACT	300
Qy	301	TTGATCCCTACAGATGAGCTATCAATGAAGAGGACATCTCTCCATGTTCTCAGCT	360
Db	301	TTGATCCCTACAGATGAGCTATCAATGAAGAGGACATCTCTCCATGTTCTCAGCT	360
Qy	361	ATCCGTTCTCAGCAGCGGTGAGCATCTGCATCAACATGCTGGCTTGGCCCGGCT	420
Db	361	ATCCGTTCTCAGCAGCGGTGAGCATCTGCATCAACATGCTGGCTTGGCCCGGCT	420
Qy	421	GACACCTGCTCTCAGGAGCAGGAGTGGTGGAGGACATGTTCAATGTGAACGTGCTG	480
Db	421	GACACCTGCTCTCAGGAGCAGGAGTGGTGGAGGACATGTTCAATGTGAACGTGCTG	480
Qy	481	GCCCTCAGCATCTGCACACGGAGGAGTACAGTCCATGAAGAGCGGATGTGGAGAT	540
Db	481	GCCCTCAGCATCTGCACACGGAGGAGTACAGTCCATGAAGAGCGGATGTGGAGAT	540
Qy	541	GGGACATCATTAACATCAATAGCATGCTGGCCACCGAGTGTACCCCTGCTGTGACC	600
Db	541	GGGACATCATTAACATCAATAGCATGCTGGCCACCGAGTGTACCCCTGCTGTGACC	600
Qy	601	CATTCTATAGTGCACCAAGATGTCGGTCACTCGGTGACAGAGGAGTCAAGCAAGAG	660
Db	601	CATTCTATAGTGCACCAAGATGTCGGTCACTCGGTGACAGAGGAGTCAAGCAAGAG	660
Qy	661	CTTGGGAGGCGGAGCCCATCGGAGCCAGTGTCTCTCCAGTGTGGTGAGACA	720
Db	661	CTTGGGAGGCGGAGCCCATCGGAGCCAGTGTCTCTCCAGTGTGGTGAGACA	720

RESULT 12

US-10-174-581-377
 ; Sequence 377, Application US/10174581
 ; Publication No. US20030017540A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.

Qy	721	CAATTGCGCTTCAAACTCCACGACGAAGGACCTCGAAGAGCGAGCTGCCACCTATGAGCAA	780
Db	721	CAATTGCGCTTCAAACTCCACGACGAAGGACCTCGAAGAGCGAGCTGCCACCTATGAGCAA	780
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Db	781	ATGAAGTGTCTCAAAACCCGAGGATGTGCCGAGGCTGTATCTAGTCTCTAGCAGCCCC	840
Qy	841	GCACATATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCGAGTGCATGAGTACTG	900
Db	841	GCACATATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCGAGTGCATGAGTACTG	900
Qy	901	TGGGAGTCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT	960
Db	901	TGGGAGTCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT	960
Qy	961	TGTTGATTTCTGGATCAGGGATACCACTTCTCTGTCACACCCGAGCGGCTAGAAA	1020
Db	961	TGTTGATTTCTGGATCAGGGATACCACTTCTCTGTCACACCCGAGCGGCTAGAAA	1020
Qy	1021	ATTGTTTGGAGTTTATATCATCTTGTCAAAATGCTTCAAGTTGTAATGTGAAAAATG	1080
Db	1021	ATTGTTTGGAGTTTATATCATCTTGTCAAAATGCTTCAAGTTGTAATGTGAAAAATG	1080
Qy	1081	GGCTGGGAAAAAGGAGGTGTCCTTAATGTTTAACTTGTGTTAACTTGTGTCCTT	1140
Db	1081	GGCTGGGAAAAAGGAGGTGTCCTTAATGTTTAACTTGTGTTAACTTGTGTCCTT	1140
Qy	1141	TGGGCACTTGGCTTTGTCGCTCTCAGTGTCTTCCCTTTCACATGGGAAAGGAGTGTG	1200
Db	1141	TGGGCACTTGGCTTTGTCGCTCTCAGTGTCTTCCCTTTCACATGGGAAAGGAGTGTG	1200
Qy	1201	GCCAAATCCCAATCTTCTTGCACCTCAACGCTCTGTGGCTCAGGGCTGGGCTGGCAGAG	1260
Db	1201	GCCAAATCCCAATCTTCTTGCACCTCAACGCTCTGTGGCTCAGGGCTGGGCTGGCAGAG	1260
Qy	1261	GAGGCTTCACTTATATCTGTGTGTTATCCAGGGCTCCAGACTTCTCTCTGCTGCTG	1320
Db	1261	GAGGCTTCACTTATATCTGTGTGTTATCCAGGGCTCCAGACTTCTCTCTGCTGCTG	1320
Qy	1321	CCCACTGACCTCTCCCTTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1380
Db	1321	CCCACTGACCTCTCCCTTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1380
Qy	1381	TCCTGTCCCTCTCTGGGCTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACCA	1440
Db	1381	TCCTGTCCCTCTCTGGGCTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACCA	1440
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Qy	1501	AAAAA 1505	
Db	1501	AAAAA 1505	


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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C41
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/10/174,581
; PRIOR FILING DATE: 2002-06-18
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/052586
; PRIOR FILING DATE: 1997-09-18
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; PRIOR APPLICATION NUMBER: 60/089105
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; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CGCGGATCGGACCCAGCAGGTGCGCGGGCGGCGGAGAGCGCGCGGGCGTCAAGTCC 60

QY 61 TCGACCCCGGTGTCGGGCTAGTCCAGCGGCGGCGGCGGCGTGGGCCCATGGCCAGG 120
DB 61 TCGACCCCGGTGTCGGGCTAGTCCAGCGGCGGCGGCGGCGTGGGCCCATGGCCAGG 120

QY 121 CCGGCGATGAGCGGTGCGCGGACCGGTGCGGCTGAGCGGGGCGCTCGGGGGGCATC 180
DB 121 CCGGCGATGAGCGGTGCGCGGACCGGTGCGGCTGAGCGGGGCGCTCGGGGGGCATC 180

QY 181 GCGCGGCGGTGGCCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
DB 181 GCGCGGCGGTGGCCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240

QY 241 ACTGTGGGCAACATCGAGGAGTGGCTGCTGAATGTAAGTGCAGGCTACCCGGGACT 300
DB 241 ACTGTGGGCAACATCGAGGAGTGGCTGCTGAATGTAAGTGCAGGCTACCCGGGACT 300

QY 301 TTGATCCCTTACAGATGACCTATCAAAAGAGGACATCCCTCTCCATGTTCTCAGCT 360
DB 301 TTGATCCCTTACAGATGACCTATCAAAAGAGGACATCCCTCTCCATGTTCTCAGCT 360

QY 361 ATCCGTTCTACGACAGCGGTGAGACATCTGCATCAACATGCTGGCTGGCCCGGCT 420
DB 361 ATCCGTTCTACGACAGCGGTGAGACATCTGCATCAACATGCTGGCTGGCCCGGCT 420

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QY 421 GACACCTGCTCTCAGCGAGCCAGTGGTTGGAAGGACATGTTCAATGTGAAGTGGCTG 480
DB 421 GACACCTGCTCTCAGCGAGCCAGTGGTTGGAAGGACATGTTCAATGTGAAGTGGCTG 480

QY 481 GCGCTCAGCATCTGCACAGCGGAAGCCTACAGTGCATGAAGGAGCGGAATGGAAGAT 540
DB 481 GCGCTCAGCATCTGCACAGCGGAAGCCTACAGTGCATGAAGGAGCGGAATGGAAGAT 540

QY 541 GGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTATACCCCTGCTGTGACC 600
DB 541 GGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTATACCCCTGCTGTGACC 600

QY 601 CACTTCTATAGTGCACCAAGTATGCGGTCACTGGCTGACAGAGGATGAGGCAAGAG 660
DB 601 CACTTCTATAGTGCACCAAGTATGCGGTCACTGGCTGACAGAGGATGAGGCAAGAG 660

QY 661 CTTGGGAGGCGGACAGACCCACATCCGAGCCAGTGCATCTCTCCAGGTGCTGGAGACA 720
DB 661 CTTGGGAGGCGGACAGACCCACATCCGAGCCAGTGCATCTCTCCAGGTGCTGGAGACA 720

QY 721 CAATTGCGCTTCAAACTCCAGCAAGGACCCCTGAGAAGGCGAGCTGCCACTATGAGCAA 780
DB 721 CAATTGCGCTTCAAACTCCAGCAAGGACCCCTGAGAAGGCGAGCTGCCACTATGAGCAA 780

QY 781 ATGAAGTGTCTCAAAACCGGAGATGTGGCGGAGGTGTATCTACGTCTCAGCACCCCC 840
DB 781 ATGAAGTGTCTCAAAACCGGAGATGTGGCGGAGGTGTATCTACGTCTCAGCACCCCC 840

QY 841 GCACACATCCAGATTGGAGACATCCAGATGAGGCCACGAGGAGCTGACCTAGTACATG 900
DB 841 GCACACATCCAGATTGGAGACATCCAGATGAGGCCACGAGGAGCTGACCTAGTACATG 900

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DB 901 TGGGAGCTCTCTCTCCCTCCCACTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960

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QY 1081 GCGTGGGAAAAGGAGGTGTCCTTAATGTTTACTTGTAACTTCTTCTGTCGCC 1140
DB 1081 GCGTGGGAAAAGGAGGTGTCCTTAATGTTTACTTGTAACTTCTTCTGTCGCC 1140

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QY 1201 GCCAAAATCCCATCTTCTTGCACCTCAACGCTGTGTGCTCAGGCTCGGGTGGCAGAGG 1260
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DB 1381 TCTTGTCCCTCTCTGGGCTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACCA 1440

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DB 1441 GGGCTGGCCAGGTGGATTTTCATGGTGATNTAAAAAGAAAAATCGAACCAAAAAA 1500

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QY 1501 AAAAA 1505
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RESULT 13
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; Sequence 377, Application US/10176483
; Publication No. US20030017541A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C68
; CURRENT APPLICATION NUMBER: US/10/176,483
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-483-377

Query Match 100.0%; Score 1505; DB 13; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CGCGATCGACCCAGAGGTGCGCGCGCGCGCGAGAGAGCGCGCGCGGTGAGCTCC 60

QY 61 TCGACCCCGGTGCTGGGCTAGTCAGAGCGAGCGCGCGCGCGCGCGCGCGCGCG 120
Db 61 TCGACCCCGGTGCTGGGCTAGTCAGAGCGAGCGCGCGCGCGCGCGCGCGCGCG 120

QY 121 CCCGCGATGAGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db 121 CCCGCGATGAGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

QY 181 GCGCGCGCGGTGCG 240
Db 181 GCGCGCGCGGTGCG 240

QY 241 ACTGTGGGCAACATCGAGAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
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QY 301 TTGATCCCCCTACAGATGTGACCTATCAATGAAGAGGACATCCTCTCCATGTTCTCAGCT 360
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QY 361 ATCCGTTCTCAGACAGCGGTGTAGACATCTGCATCAAAATGCTGGCTTGGCGCGGCT 420
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Db 421 GACACCTCTCTCAGGAGCACCGAGTGTGGAAGGACATGTTCAATGTAACGTGCTG 480

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Db 481 GGCCTCAGCATCTGCACAGCGGAGCGCTACCGATCCATGAAGAGCGGGAATGTGGACGAT 540

QY 541 GGCACATCATTAACATAGATGCTGGCCACCGAGTGTACCCCTCTCTGTGACC 600
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QY 601 CACTTCTATAGTGCACCAAGATATGCGCTCACTGCGCTGACAGAGGAGCTGAGCAAGAG 660
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QY 781 ATGAAGTGTCTCAAAACCGAGGATGTGGCGAGGCTGTTATCTACGCTCTCAGACCCGCC 840
Db 781 ATGAAGTGTCTCAAAACCGAGGATGTGGCGAGGCTGTTATCTACGCTCTCAGACCCGCC 840

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GenCore version 5.1.6
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(without alignments)
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Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 212409041 residues

Word size : 10

Total number of hits satisfying chosen parameters: 2278698

Minimum DB seq length: 0
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1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002s.*
7: Geneseq2003as.*
8: Geneseq2003bs.*
9: Geneseq2003cs.*
10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1505	100.0	1505	4	AAS46113	AAS46113 Human PRO
2	1505	100.0	1505	4	AAS46113	AAS46113 Human PRO
3	1505	100.0	1505	6	ABX74441	ABX74441 Human CDN
4	1505	100.0	1505	7	ABX78716	ABX78716 Human PRO
5	1505	100.0	1505	7	ACA75688	ACA75688 Novel hum
6	1505	100.0	1505	7	ACA71168	ACA71168 Human sec
7	1505	100.0	1505	7	ACC87696	ACC87696 Human sec
8	1505	100.0	1505	7	ACC87082	ACC87082 Human sec
9	1505	100.0	1505	7	ACD04255	ACD04255 Human sec
10	1505	100.0	1505	7	ACA69586	ACA69586 cDNA enco
11	1505	100.0	1505	7	ACA90431	ACA90431 Novel hum
12	1505	100.0	1505	7	ACC89538	ACC89538 Human sec
13	1505	100.0	1505	7	ACA98329	ACA98329 Novel hum
14	1505	100.0	1505	7	ACA93971	ACA93971 Human sec
15	1505	100.0	1505	7	ACD15364	ACD15364 Human sec
16	1505	100.0	1505	7	ACD08951	ACD08951 Human sec
17	1505	100.0	1505	7	ACC96871	ACC96871 Human sec
18	1505	100.0	1505	7	ACF15592	ACF15592 Human sec
19	1505	100.0	1505	7	ACA72959	ACA72959 Human PRO
20	1505	100.0	1505	7	ACD03131	ACD03131 Novel hum
21	1505	100.0	1505	7	ACD01946	ACD01946 Novel hum
22	1505	100.0	1505	7	ACA92138	ACA92138 Novel hum
23	1505	100.0	1505	7	ACA89563	ACA89563 cDNA enco

ALIGNMENTS

RESULT 1	
AAS46113	
ID	AAS46113 standard; cDNA; 1505 BP.
XX	
AC	AAS46113;
XX	
DT	18-DEC-2001 (first entry)
XX	
XX	Human DNA encoding PRO polypeptide sequence #189.
XX	
KW	dog polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW	dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW	blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW	adrenal; lung; breast; prostate; cervix; liver; genetic disorder;
KW	PCR primer.
XX	
OS	Homo sapiens.
XX	
PN	WO200168948-A2.
XX	
PD	20-SEP-2001.
XX	
PF	28-FEB-2001; 2001WO-US006520.
XX	
XX	
PR	01-MAR-2000; 2000WO-US005601.
PR	02-MAR-2000; 2000WO-US005841.
PR	03-MAR-2000; 2000US-0187202P.
PR	06-MAR-2000; 2000US-0186968P.
PR	14-MAR-2000; 2000US-0189320P.
PR	14-MAR-2000; 2000US-0189328P.
PR	15-MAR-2000; 2000WO-US006884.
PR	21-MAR-2000; 2000US-0190828P.
PR	21-MAR-2000; 2000US-0191007P.
PR	21-MAR-2000; 2000US-0191048P.
PR	21-MAR-2000; 2000US-0191314P.
PR	28-MAR-2000; 2000US-0192655P.
PR	29-MAR-2000; 2000US-0193032P.
PR	29-MAR-2000; 2000US-0193053P.
PR	30-MAR-2000; 2000WO-US008439.
PR	04-APR-2000; 2000US-0194449P.
PR	04-APR-2000; 2000US-0194647P.
PR	11-APR-2000; 2000US-0195975P.
PR	11-APR-2000; 2000US-0196000P.
PR	11-APR-2000; 2000US-0196187P.
PR	11-APR-2000; 2000US-0196690P.
PR	11-APR-2000; 2000US-0196820P.

ACA73573 Human sec
ACA05888 Human sec
ACA66722 CDNA enco
ACA91227 Novel hum
ACD81604 Human CDN
ACF20297 Human sec
ACF19683 Human sec
ACD21971 Human sec
ACF13136 Human sec
ACD25239 Human sec
ACF00288 Human sec
ACA60426 Novel hum
ACA72345 Novel hum
ACD04869 Novel hum
ACD18330 Human sec
ACD08337 Human sec
ACA88771 Novel hum
ACA70213 Human sec
ACD12435 Novel hum
ACC74350 Human sec
ACD15978 Human sec
ACD25546 Novel hum

PR 18-APR-2000; 2000US-0198121P.
 PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199654P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 PI P-PSDB; AAU29212.
 XX WPI; 2001-602746/68.
 DR
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX
 XX Claim 2; Fig 377; 774pp; English.
 PS
 XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
 CC primers for PRO polypeptides of the invention. The sequences of the
 CC invention can be used to detect the presence of a tumour in a mammal by
 CC comparing the level of expression of a PRO polypeptide in a test sample
 CC of cells from the animal and a control sample of normal cells, whereby a
 CC higher level of expression in the test sample indicates the presence of a
 CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be
 CC used to stimulate tumour necrosis factor (TNF) alpha release from human
 CC blood, when contacted with it. A specific polypeptide can be used to
 CC stimulate the proliferation or differentiation of chondrocyte cells. The
 CC PRO proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX
 XX Sequence 1505 BP; 309 A; 442 C; 419 G; 335 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 1505; DB 4; Length 1505;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGCGATCGGACCCAAAGCAGGTTCGCGCGCGCGGAGAGAGCGCGCGGCGTCAAGTCC 60
 DB 1 CGCGATCGGACCCAAAGCAGGTTCGCGCGCGCGGAGAGAGCGCGCGGCGTCAAGTCC 60
 QY 61 TCGACCCCGGTGTCGGGTAGTTCAGAGAGCGGACCGGCGCGTGGGCCCATGGCCAGG 120
 DB 61 TCGACCCCGGTGTCGGGTAGTTCAGAGAGCGGACCGGCGCGTGGGCCCATGGCCAGG 120
 QY 121 CCCGCGATGGAGCGGTGCGGACCGGTGCGGTGAGCGGGCCCTCGGGGGGCATC 180
 DB 121 CCCGCGATGGAGCGGTGCGGACCGGTGCGGTGAGCGGGCCCTCGGGGGGCATC 180
 QY 181 GCGCGCGCGGTGCGGCGCGGTGAGCGAGGAGTGAAGGTGGTGGGCTGGCGCCGC 240
 DB 181 GCGCGCGCGGTGCGGCGCGGTGAGCGAGGAGTGAAGGTGGTGGGCTGGCGCCGC 240
 QY 241 ACTTGGGCACATCGAGAGTGGTCTGTAATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 300
 DB

DB 241 ACTTGGGGCAACATCGAGAGGTGGTCTGTAATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 300
 QY 301 TTGATCCCTACAGATGTGACCTATCAAAATGAAGAGGACATCTCTTCCATGTTCTCAGCT 360
 DB 301 TTGATCCCTACAGATGTGACCTATCAAAATGAAGAGGACATCTCTTCCATGTTCTCAGCT 360
 QY 361 ATCCGTTCTCAGACAGCGGTGTAGACATCTGCATCAACAATGCTGGTGGTGGCCCGCT 420
 DB 361 ATCCGTTCTCAGACAGCGGTGTAGACATCTGCATCAACAATGCTGGTGGTGGCCCGCT 420
 QY 421 GACACCTGCTCTCAGGAGCAGCAGTGTGCGAAGGACATCTCAATCTGAACGTCG 480
 DB 421 GACACCTGCTCTCAGGAGCAGCAGTGTGCGAAGGACATCTCAATCTGAACGTCG 480
 QY 481 GGCCTCAGCATCTGCACACGGGAAGCCTACCAAGTCCATGAAGAGCGGAATGTGGACGAT 540
 DB 481 GGCCTCAGCATCTGCACACGGGAAGCCTACCAAGTCCATGAAGAGCGGAATGTGGACGAT 540
 QY 541 GGGCACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACC 600
 DB 541 GGGCACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACC 600
 QY 601 CACTTCTATAGTGCACCAAGTATCCGTCAGTGCCTGACAGAGAGGACATGAGGCAAGAG 660
 DB 601 CACTTCTATAGTGCACCAAGTATCCGTCAGTGCCTGACAGAGGACTGAGGCAAGAG 660
 QY 661 CTTGGGAGGCCAGACCCACATCCAGGCCAGTGCATCTCTCCAGGTGTGTGGAGACA 720
 DB 661 CTTGGGAGGCCAGACCCACATCCAGGCCAGTGCATCTCTCCAGGTGTGTGGAGACA 720
 QY 721 CAATTCGGCTTCAAACTCCAGCAGAGGACCTGAGAGGAGGAGTGCACCTATGAGCA 780
 DB 721 CAATTCGGCTTCAAACTCCAGCAGAGGACCTGAGAGGAGGAGTGCACCTATGAGCA 780
 QY 781 ATGAAGTGTCTCAAAACCCGAGGATGTGGCGAGGTGTATCTAGTCTCTCAGCACCC 840
 DB 781 ATGAAGTGTCTCAAAACCCGAGGATGTGGCGAGGTGTATCTAGTCTCTCAGCACCC 840
 QY 841 GCACATCCAGATTTGGAGACATCCAGATGAGGCCACCGAGAGGAGTGCACCTAGTACTG 900
 DB 841 GCACATCCAGATTTGGAGACATCCAGATGAGGCCACCGAGAGGAGTGCACCTAGTACTG 900
 QY 901 TGGGAGCTCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 960
 DB 901 TGGGAGCTCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 960
 QY 961 TGTGATTTCTGGATCAGGGATACCACTTCTGTCCACACCCGAGGAGGAGTGAAGAA 1020
 DB 961 TGTGATTTCTGGATCAGGGATACCACTTCTGTCCACACCCGAGGAGGAGTGAAGAA 1020
 QY 1021 ATTTGTTGAGATTTTATATCATCTTGTCAAAATGCTTCAAGTGTGTAATGTGAAAAATG 1080
 DB 1021 ATTTGTTGAGATTTTATATCATCTTGTCAAAATGCTTCAAGTGTGTAATGTGAAAAATG 1080
 QY 1081 GGCTGGGAAAGAGGAGTGTCTCCCTAACTTTTACTTTTACTTTTACTTTTACTTTTACTTT 1140
 DB 1081 GGCTGGGAAAGAGGAGTGTCTCCCTAACTTTTACTTTTACTTTTACTTTTACTTTTACTTT 1140
 QY 1141 TGGGACATTTGGCCCTTTGTCT 1200
 DB 1141 TGGGACATTTGGCCCTTTGTCT 1200
 QY 1201 GCCAAATCCCATCTTCTTGCACCTCAACGCTCTGTGGCTCAGGGCTGGGGTGGCAGAGG 1260
 DB 1201 GCCAAATCCCATCTTCTTGCACCTCAACGCTCTGTGGCTCAGGGCTGGGGTGGCAGAGG 1260
 QY 1261 GAGGCTTCACTTTATATCTGTGTTGTTATCCAGGGCTCCAGACTTCTCTCTCTCTCTCTCT 1320
 DB 1261 GAGGCTTCACTTTATATCTGTGTTGTTATCCAGGGCTCCAGACTTCTCTCTCTCTCTCTCT 1320
 QY 1321 CCCACTGACCCCTCTCCCCCTTATCTATCTCTTCTCGGCTCCCGAGCCAGCTCTTGCT 1380
 DB 1321 CCCACTGACCCCTCTCCCCCTTATCTATCTCTTCTCGGCTCCCGAGCCAGCTCTTGCT 1380

QY 1381 TCTGTGTCCTCTGGGGTATCCCTCCACTCTGACTCTGACTATGGCAGAGAACCA 1440
Db TCTTGTCCCTCTCTGGGGTATCCCTCCACTCTGACTCTGACTATGGCAGAGAACCA 1440
QY 1441 GGGCTGCCCCAGTGGATTTCATGTGTATCATTAAGAAAGAAATCGAACCAAAAAA 1500
Db 1441 GGGCTGCCCCAGTGGATTTCATGTGTATCATTAAGAAAGAAATCGAACCAAAAAA 1500
QY 1501 AAAAA 1505
Db 1501 AAAAA 1505

RESULT 2
AAF92121
ID AAF92121 standard; cDNA; 1505 BP.

AC AAF92121;
XX
DT 15-MAY-2001 (first entry)
XX Human PRO1774 cDNA.
DE
XX Human; PRO protein; mapping; ss.
KW
XX Homo sapiens.
OS
XX WO200116318-A2.
PN
PD 08-MAR-2001.

XX 24-AUG-2000; 2000WO-US023328.

XX 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 01-MAR-2000; 2000WO-US005601.
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000WO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.

XX (GETH) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;

XX WPI; 2001-183260/18.
DR P-PsDB; AAB87589.

PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.

XX Claim 2; Fig 127; 279pp; English.

XX The present sequence is the coding sequence for a human PRO polypeptide
CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC antagonists or anti-PRO antibodies are useful for preparation of a
CC medicament useful in the treatment of a condition which is responsive to
CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC protein may also be employed as molecular weight markers for protein
CC electrophoresis. The PRO coding sequence has applications in molecular
CC biology, including use as hybridisation probes, and in chromosome and
CC gene mapping

XX Sequence 1505 BP; 309 A; 442 C; 419 G; 335 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1505; DB 4; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCGATCGACCCAGCAGSTCGCGCGCGCGCAGGAGAGCGGCCGGGCGTCACTCC 60
Db 1 CGCGATCGACCCAGCAGSTCGCGCGCGCGCAGGAGAGCGGCCGGGCGTCACTCC 60
QY 61 TCGACCCCGCGTGTGGGCTAGTCCAGCGAGCGGACGGCGCGCTGGGCCCATGCCAGG 120
Db 61 TCGACCCCGCGTGTGGGCTAGTCCAGCGAGCGGAGCGGCGCGCTGGGCCCATGCCAGG 120
QY 121 CCGGCATGGAGCGGTGGCGCGACCGGCTGCGTGTGACCGGGGCGCTCGGGGGGCATC 180
Db 121 CCGGCATGGAGCGGTGGCGCGACCGGCTGCGTGTGACCGGGGCGCTCGGGGGGCATC 180
QY 181 GCGCGCGCGTGGCGCGCGCGCGCGCGCTGGTCCAGCAGGACTGAAGGTGGTGGCGCGC 240
Db 181 GCGCGCGCGTGGCGCGCGCGCGCGCGCTGGTCCAGCAGGACTGAAGGTGGTGGCGCGC 240
QY 241 ACTGTGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGACT 300
Db 241 ACTGTGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGACT 300
QY 301 TTGATCCCTACAGATGACCTATCAAAATGAAGGACATCTCTTCCATTTCTCAGCT 360
Db 301 TTGATCCCTACAGATGACCTATCAAAATGAAGGACATCTCTTCCATTTCTCAGCT 360
QY 361 ATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGGCTGGCGCGGCT 420
Db 361 ATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGGCTGGCGCGGCT 420
QY 421 GACACCTGCTCTCAGGCGACACAGTGGTGGAGGACATGTTCAATGTCAACGTGCTG 480
Db 421 GACACCTGCTCTCAGGCGACACAGTGGTGGAGGACATGTTCAATGTCAACGTGCTG 480
QY 481 GCCCTCAGCATCTGCACACGGGAGCCTACCAAGTCCATGAAGGAGCGGAAATGTGACAT 540
Db 481 GCCCTCAGCATCTGCACACGGGAGCCTACCAAGTCCATGAAGGAGCGGAAATGTGACAT 540
QY 541 GGGCAGCATNTAATCAATAGCATGTCTGGCCACCGAGTGTACCCCTCTCTGTGACC 600
Db 541 GGGCAGCATNTAATCAATAGCATGTCTGGCCACCGAGTGTACCCCTCTCTGTGACC 600
QY 601 CACTTCTATAGTGCCACCAAGTATGCCGTCACTGGCTGACAGAGGAGCTGAGGCAAGAG 660
Db 601 CACTTCTATAGTGCCACCAAGTATGCCGTCACTGGCTGACAGAGGAGCTGAGGCAAGAG 660
QY 661 CTTGGGAGGCCAGACCCACATCCGAGCCAGTGCATCTCTCCAGGTGTGTGGAGACA 720
Db 661 CTTGGGAGGCCAGACCCACATCCGAGCCAGTGCATCTCTCCAGGTGTGTGGAGACA 720
QY 721 CAATTGCGCTTCAAACTCCAGCAGAACCCCTGAGAGGCGAGTCCACCTATGAGCAA 780
Db 721 CAATTGCGCTTCAAACTCCAGCAGAACCCCTGAGAGGCGAGTCCACCTATGAGCAA 780
QY 781 ATGAAGTGTCTCAAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCTCAGCAGCC 840
Db 781 ATGAAGTGTCTCAAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCTCAGCAGCC 840
QY 841 GCACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCAGGTGACCTAGTGA 900
Db 841 GCACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCAGGTGACCTAGTGA 900
QY 901 TGGGAGCTCCTCTTCCCTCCACCTTCAATGGCTTGCCTCTCCCTCTGGATTTAGG 960
Db 901 TGGGAGCTCCTCTTCCCTCCACCTTCAATGGCTTGCCTCTCCCTCTGGATTTAGG 960
QY 961 TGTTGATTTCTTGATTCAGGGATACCACTTCTCTGTCACACCCCGACCGAGGGCTAGAAA 1020
Db 961 TGTTGATTTCTTGATTCAGGGATACCACTTCTCTGTCACACCCCGACCGAGGGCTAGAAA 1020

Db 961 TGTGATTTCTGGATCAGCGGATACCACTTCCTGTCACACCCGACCGGGCTAGAAA 1020
 QY 1021 ATTGTTTTCAGATTTTATATCATCTTGCAATGCTTCAGTTGTAATGTGAAAAATG 1080
 Db 1021 ATTGTTTTCAGATTTTATATCATCTTGCAATGCTTCAGTTGTAATGTGAAAAATG 1080
 QY 1081 GCGTGGGGAAGAGAGTGTGCTCCCTAAATGTTTACTTGTAACTTGTCTTGCGCCC 1140
 Db 1081 GCGTGGGGAAGAGAGTGTGCTCCCTAAATGTTTACTTGTAACTTGTCTTGCGCCC 1140
 QY 1141 TGGGCACTTGGCTTTTGTCTGCTCTCAGTGTCTTCCCTTGACATGGGAAAGAGTTGTG 1200
 Db 1141 TGGGCACTTGGCTTTTGTCTGCTCTCAGTGTCTTCCCTTGACATGGGAAAGAGTTGTG 1200
 QY 1201 GCCAAATCCCATCTTCTTGCACTCAACGCTCTGCGCTCAGGGCTGGGGTGGCAGAG 1260
 Db 1201 GCCAAATCCCATCTTCTTGCACTCAACGCTCTGCGCTCAGGGCTGGGGTGGCAGAG 1260
 QY 1261 GAGGCTTCCACCTTATCTGTGTGTATCCAGGCTCCAGACTTCCTCTCTGCTGCTG 1320
 Db 1261 GAGGCTTCCACCTTATCTGTGTGTATCCAGGCTCCAGACTTCCTCTCTGCTGCTG 1320
 QY 1321 CCCACTGACCTCTCCCTCTATCTATCTCTTCTGCTCCAGCCAGCTCTTGGCT 1380
 Db 1321 CCCACTGACCTCTCCCTCTATCTATCTCTTCTGCTCCAGCCAGCTCTTGGCT 1380
 QY 1381 TCTTCTCCCTCTGCGGTCACTCCCTCCACTCTGACTCTGACTATGGCAGCAGACCA 1440
 Db 1381 TCTTCTCCCTCTGCGGTCACTCCCTCCACTCTGACTCTGACTATGGCAGCAGACCA 1440
 QY 1441 GGGCTGCGCCAGTGGATTCATGTGTGATCAATAAAAAAGAAAAATCGCAACCAAAAA 1500
 Db 1441 GGGCTGCGCCAGTGGATTCATGTGTGATCAATAAAAAAGAAAAATCGCAACCAAAAA 1500
 QY 1501 AAAAA 1505
 Db 1501 AAAAA 1505

RESULT 3

ABS74441
 ID ABS74441 standard; cDNA; 1505 BP.
 XX
 AC ABS74441;
 DT
 TT
 XX 10-DEC-2002 (first entry)
 DE Human cDNA encoding secreted/transmembrane protein PRO1774.
 KW Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;
 KW antiarthritic; osteopathic; sports-related joint problem;
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US2002119130-A1.
 XX
 PD 29-AUG-2002.
 XX
 PF 06-DEC-2001; 2001US-00006867.
 XX
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 22-APR-1998; 98US-0082797P.
 PR 29-APR-1998; 98US-0083495P.
 PR 15-MAY-1998; 98US-0085579P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088030P.
 PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088740P.
 PR 10-JUN-1998; 98US-0088811P.

PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088825P.
 PR 11-JUN-1998; 98US-0088863P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089553P.
 PR 19-JUN-1998; 98US-0089952P.
 PR 22-JUN-1998; 98US-0090246P.
 PR 24-JUN-1998; 98US-0090444P.
 PR 25-JUN-1998; 98US-0090688P.
 PR 26-JUN-1998; 98US-0090862P.
 PR 02-JUL-1998; 98US-0091628P.
 PR 10-AUG-1998; 98US-0096012P.
 PR 17-AUG-1998; 98US-0096757P.
 PR 18-AUG-1998; 98US-0096949P.
 PR 18-AUG-1998; 98US-0096959P.
 PR 26-AUG-1998; 98US-0097954P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 26-AUG-1998; 98US-0097979P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099815P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 22-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 30-SEP-1998; 98US-0101916P.
 PR 06-OCT-1998; 98US-0102570P.
 PR 08-MAR-1999; 98US-0103449P.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021194.
 PR 22-DEC-1999; 99WO-US030720.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032378.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019892.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX WPI; 2002-731348/79.
 DR P-FSDB; ABG95914.

XX New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX Claim 2; Fig 127; 399pp; English.
XX The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95951-ABG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence encodes a novel secreted or transmembrane protein of the
XX invention
XX
SQ Sequence 1505 BP; 309 A; 442 C; 419 G; 335 T; 0 U; 0 Other;
Query Match 100.0%; Score 1505; DB 6; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCGATCGGACCCAGAGCTCGCGCGCGCGCGCGAGAGAGCGCGCGCGTACAGTCC 60
DB |||||
QY 1 CGCGATCGGACCCAGAGCTCGCGCGCGCGCGCGAGAGAGCGCGCGCGTACAGTCC 60
DB |||||
QY 61 TCGACCCCGGTGTCGGGTAGTCCAGCAGGCGGCGCGCGCGCGTGGGCCATGCCAGG 120
DB |||||
QY 61 TCGACCCCGGTGTCGGGTAGTCCAGCAGGCGGCGCGCGCGTGGGCCATGCCAGG 120
DB |||||
QY 121 CCCGCGATGGAGCGGTGGCGGACCGGTGGCGGTGGTGAACCGGGGCGTTCGGGGGGC 180
DB |||||
QY 121 CCCGCGATGGAGCGGTGGCGGACCGGTGGCGGTGGTGAACCGGGGCGTTCGGGGGGC 180
DB |||||
QY 181 GCGCGGCGGTGGCGGCGCGTGGTCCAGCAGGAGCTGAAGTGGTGGCTGGCGCGGC 240
DB |||||
QY 181 GCGCGGCGGTGGCGGCGCGTGGTCCAGCAGGAGCTGAAGTGGTGGCTGGCGCGGC 240
DB |||||
QY 241 ACTGTGGGCAACATCGAGAGCTGGCTGCTGAATGTGAAGTGAAGTGAAGTGAAGT 300
DB |||||

Db 241 ACTGTGGGCAACATCGAGGAGCTGGCTGCTGAATGTGAAGTGAAGTGAAGTGAAGT 300
QY 301 TTGATCCCTACAGATGTGACCTATCAATGAAGAGGACATCCCTCTCCATGTTCTCAGCT 360
DB |||||
QY 301 TTGATCCCTACAGATGTGACCTATCAATGAAGAGGACATCCCTCTCCATGTTCTCAGCT 360
DB |||||
QY 361 ATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACATGCTGGCTGGCGCGGCT 420
DB |||||
QY 361 ATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACATGCTGGCTGGCGCGGCT 420
DB |||||
QY 421 GACACCTCTCTCAGGAGCAGCAGTGGTGGAGGACATGTTCAATGTGAACGTCGTG 480
DB |||||
QY 421 GACACCTCTCTCAGGAGCAGCAGTGGTGGAGGACATGTTCAATGTGAACGTCGTG 480
DB |||||
QY 481 GCCCTCAGCATCTGCACAGGGAAGCCTACAGTCCATGAAGAGGCGGAATGTGAGCAT 540
DB |||||
QY 481 GCCCTCAGCATCTGCACAGGGAAGCCTACAGTCCATGAAGAGGCGGAATGTGAGCAT 540
DB |||||
QY 541 GGGCACATCATTAACATCAATAGCATGTGCGCCACCGAGTGTACCCCTCTCTGTGACC 600
DB |||||
QY 541 GGGCACATCATTAACATCAATAGCATGTGCGCCACCGAGTGTACCCCTCTCTGTGACC 600
DB |||||
QY 601 CACTTCTATAGTGGCCACCAAGTATGCGCTCACTCGGTGACAGAGGAGTCAAGCAAGAG 660
DB |||||
QY 601 CACTTCTATAGTGGCCACCAAGTATGCGCTCACTCGGTGACAGAGGAGTCAAGCAAGAG 660
DB |||||
QY 661 CTTGGGAGGCGGAGAGCCACATCGAGCCAGTGCATCTCTCCAGGTGTGGTGAGACA 720
DB |||||
QY 661 CTTGGGAGGCGGAGAGCCACATCGAGCCAGTGCATCTCTCCAGGTGTGGTGAGACA 720
DB |||||
QY 721 CAATTTGGCTTTCAAACTCCAGCAAGGACCTGAGAGGCGAGTGCACCTATGAGCAA 780
DB |||||
QY 721 CAATTTGGCTTTCAAACTCCAGCAAGGACCTGAGAGGCGAGTGCACCTATGAGCAA 780
DB |||||
QY 781 ATGAAGTGTCTCAAACTCCAGGAGTGTGCGCGAGGCTGTATCTACGTCTCAGCACCC 840
DB |||||
QY 781 ATGAAGTGTCTCAAACTCCAGGAGTGTGCGCGAGGCTGTATCTACGTCTCAGCACCC 840
DB |||||
QY 841 GCACATCCAGATGGAGACATCCAGTGAAGGCCACCGGAGGAGTCACTAGTACGTG 900
DB |||||
QY 841 GCACATCCAGATGGAGACATCCAGTGAAGGCCACCGGAGGAGTCACTAGTACGTG 900
DB |||||
QY 901 TGGGAGCTCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 960
DB |||||
QY 901 TGGGAGCTCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 960
DB |||||
QY 961 TGTTCATTTCTGGATCAGGAGTACCACTTCTCTGTCACACCCCGACCGAGGCTAGAAA 1020
DB |||||
QY 961 TGTTCATTTCTGGATCAGGAGTACCACTTCTCTGTCACACCCCGACCGAGGCTAGAAA 1020
DB |||||
QY 1021 ATTTGTTGAGATTTTATATCATCTGTCAAAATGCTTCAAGTGTGAATGTGAATAATG 1080
DB |||||
QY 1021 ATTTGTTGAGATTTTATATCATCTGTCAAAATGCTTCAAGTGTGAATGTGAATAATG 1080
DB |||||
QY 1081 GGCTGGGGAAGAGGAGTGGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1140
DB |||||
QY 1081 GGCTGGGGAAGAGGAGTGGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1140
DB |||||
QY 1141 TGGGCACCTTGGCTTTGCTCTCTCAGTGTCTTCCCTTTTTCACATGGGAAAGGAGTGTG 1200
DB |||||
QY 1141 TGGGCACCTTGGCTTTGCTCTCTCAGTGTCTTCCCTTTTTCACATGGGAAAGGAGTGTG 1200
DB |||||
QY 1201 GCCAAATCCCATCTTCTTTCGACCTCAACGTCTGTGGCTCAGGGCTGGGGTGGCAGAGG 1260
DB |||||
QY 1201 GCCAAATCCCATCTTCTTTCGACCTCAACGTCTGTGGCTCAGGGCTGGGGTGGCAGAGG 1260
DB |||||
QY 1261 GAGGCTTCACTTATATCTGTGTGTGTATTCAGGGCTCCAGACTTCTCTCTCTGCTGCTG 1320
DB |||||
QY 1261 GAGGCTTCACTTATATCTGTGTGTGTATTCAGGGCTCCAGACTTCTCTCTGCTGCTG 1320
DB |||||
QY 1321 CCCACTGACCCCTCTCCCTCTTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
DB |||||
QY 1321 CCCACTGACCCCTCTCTCTCTTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
DB |||||

QY	1381	TCCTGTCCTCCCTCTGGGGTCATCCCTCCACTCTGTGACTCTGACTATGCAGACCA	1440
Db	1381	TCCTGTCCTCCCTCTGGGGTCATCCCTCCACTCTGACTCTGACTATGCAGACCA	1440
QY	1441	GGGCGCTGGCCAGTCGGATTTTCATGGTGATCATTTAAAAAGAAAAATCGCAACCAAAAA	1500
Db	1441	GGGCGCTGGCCAGTCGGATTTTCATGGTGATCATTTAAAAAGAAAAATCGCAACCAAAAA	1500
QY	1501	AAAAA 1505	
Db	1501	AAAAA 1505	
RESULT 4			
ABX78716			
ID	ABX78716	standard; cDNA; 1505 BP.	
XX	AC	ABX78716;	
XX	XX		
DT	15-APR-2003	(first entry)	
XX	XX	Human PRO polynucleotide #189.	
KW	Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;		
KW	liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;		
KW	antibody-dependent enzyme mediated prodrug therapy.		
OS	Homo sapiens.		
PN	US2003027272-A1.		
PD	06-FEB-2003.		
XX	XX		
XX	21-JUN-2002;	2002US-00176492.	
PR	18-SRP-1997;	97US-0059263P.	
PR	18-SRP-1997;	97US-0059266P.	
PR	17-OCT-1997;	97US-0062250P.	
PR	21-OCT-1997;	97US-0063486P.	
PR	24-OCT-1997;	97US-0063120P.	
PR	24-OCT-1997;	97US-0063121P.	
PR	28-OCT-1997;	97US-0063540P.	
PR	28-OCT-1997;	97US-0063541P.	
PR	28-OCT-1997;	97US-0063544P.	
PR	28-OCT-1997;	97US-0063564P.	
PR	29-OCT-1997;	97US-0063734P.	
PR	31-OCT-1997;	97US-0063870P.	
PR	31-OCT-1997;	97US-0064103P.	
PR	13-NOV-1997;	97US-0065311P.	
PR	21-NOV-1997;	97US-0066120P.	
PR	24-NOV-1997;	97US-0066466P.	
PR	24-NOV-1997;	97US-0066772P.	
PR	11-DEC-1997;	97US-0069335P.	
PR	12-DEC-1997;	97US-0069425P.	
PR	17-DEC-1997;	97US-0069870P.	
PR	18-DEC-1997;	97US-0068017P.	
PR	10-MAR-1998;	98US-0077450P.	
PR	11-MAR-1998;	98US-0077632P.	
PR	11-MAR-1998;	98US-0077649P.	
PR	20-MAR-1998;	98US-0077886P.	
PR	20-MAR-1998;	98US-0078939P.	
PR	27-MAR-1998;	98US-0079664P.	
PR	27-MAR-1998;	98US-0079786P.	
PR	31-MAR-1998;	98US-0080107P.	
PR	31-MAR-1998;	98US-0080194P.	
PR	01-APR-1998;	98US-0080327P.	
PR	01-APR-1998;	98US-0080333P.	
PR	08-APR-1998;	98US-0081049P.	
PR	08-APR-1998;	98US-0081070P.	
PR	09-APR-1998;	98US-0081195P.	
PR	15-APR-1998;	98US-0081838P.	
PR	21-APR-1998;	98US-0082568P.	
PR	21-APR-1998;	98US-0082569P.	
PR	22-APR-1998;	98US-0082704P.	
PR	22-APR-1998;	98US-0082797P.	
PR	28-APR-1998;	98US-0083322P.	
PR	29-APR-1998;	98US-0083495P.	
PR	29-APR-1998;	98US-0083496P.	
PR	29-APR-1998;	98US-0083499P.	
PR	29-APR-1998;	98US-0083559P.	
PR	05-MAY-1998;	98US-0084366P.	
PR	06-MAY-1998;	98US-0084414P.	
PR	07-MAY-1998;	98US-0084639P.	
PR	07-MAY-1998;	98US-0084640P.	
PR	07-MAY-1998;	98US-0084643P.	
PR	15-MAY-1998;	98US-0085579P.	
PR	15-MAY-1998;	98US-0085580P.	
PR	15-MAY-1998;	98US-0085582P.	
PR	15-MAY-1998;	98US-0085700P.	
PR	18-MAY-1998;	98US-0086023P.	
PR	22-MAY-1998;	98US-0086392P.	
PR	22-MAY-1998;	98US-0086486P.	
PR	28-MAY-1998;	98US-0087098P.	
PR	28-MAY-1998;	98US-0087208P.	
PR	02-JUN-1998;	98US-0087609P.	
PR	02-JUN-1998;	98US-0087759P.	
PR	03-JUN-1998;	98US-0087827P.	
PR	04-JUN-1998;	98US-0088025P.	
PR	04-JUN-1998;	98US-0088028P.	
PR	04-JUN-1998;	98US-0088029P.	
PR	04-JUN-1998;	98US-0088033P.	
PR	04-JUN-1998;	98US-0088326P.	
PR	05-JUN-1998;	98US-0088167P.	
PR	0		

[illegible]

QY	1081	GGCTGGGGAAGAGGTGGTCCCTAAATGTTTACTTTGTTAACTGTTCTTGTCGCC	1140	PR	24-NOV-1997;	97US-0066466P.
Db	1081	GGCTGGGGAAGAGGTGGTCCCTAAATGTTTACTTTGTTAACTGTTCTTGTCGCC	1140	PR	24-NOV-1997;	97US-0066772P.
QY	1141	TGGGCACCTTGGCCTTTGTCTGTCTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGTTGTG	1200	PR	11-DEC-1997;	97US-0069333P.
Db	1141	TGGGCACCTTGGCCTTTGTCTGTCTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGTTGTG	1200	PR	12-DEC-1997;	97US-0069425P.
QY	1201	GCAGAAATCCCATCTTCTTGACACCTCAACGCTGTGGCTCAGGGCTGGGGTGGCAGAGG	1260	PR	17-DEC-1997;	97US-0069870P.
Db	1201	GCAGAAATCCCATCTTCTTGACACCTCAACGCTGTGGCTCAGGGCTGGGGTGGCAGAGG	1260	PR	18-DEC-1997;	97US-0068017P.
QY	1261	GAGGCTTCACCTTATATCTGTGTCTTATCCAGGCTCCAGACTTCCTCCTCTGCCTCG	1320	PR	10-MAR-1998;	98US-0077450P.
Db	1261	GAGGCTTCACCTTATATCTGTGTCTTATCCAGGCTCCAGACTTCCTCCTCTGCCTCG	1320	PR	11-MAR-1998;	98US-0077632P.
QY	1321	CCCACTGCACCTCTCCCTTATCTATCTCTCTCGGCTCCCAAGCCAGCTTTGGCT	1380	PR	11-MAR-1998;	98US-0077649P.
Db	1321	CCCACTGCACCTCTCCCTTATCTATCTCTCTCGGCTCCCAAGCCAGCTTTGGCT	1380	PR	20-MAR-1998;	98US-0078886P.
QY	1381	TCCTGCTCCCTCTGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACCA	1440	PR	20-MAR-1998;	98US-0078939P.
Db	1381	TCCTGCTCCCTCTGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACCA	1440	PR	27-MAR-1998;	98US-0079664P.
QY	1441	GGGCTGGCCAGTGGATTTCATGGTGATCATTTAAAGAAAAATCGCAACCAAAAA	1500	PR	31-MAR-1998;	98US-0080107P.
Db	1441	GGGCTGGCCAGTGGATTTCATGGTGATCATTTAAAGAAAAATCGCAACCAAAAA	1500	PR	01-APR-1998;	98US-0080194P.
QY	1501	AAAAA 1505		PR	01-APR-1998;	98US-0080327P.
Db	1501	AAAAA 1505		PR	01-APR-1998;	98US-0080333P.
RESULT 5						98US-0081049P.
ID	ACA75688	standard; cdNA; 1505 BP.				98US-0081070P.
AC	ACA75688;					98US-0081195P.
XX						98US-0081838P.
DT	07-JUL-2003	(first entry)				98US-0082568P.
DE						98US-0082569P.
KW	Human; secreted and transmembrane protein PRO1774 cdNA.					98US-0082704P.
KW	tumour necrosis factor-alpha release; TNF-alpha release;					98US-0082797P.
KW	chondrocyte proliferation; chondrocyte differentiation; tumour;					98US-0083322P.
KW	adrenal tumour; lung tumour; colon tumour; breast tumour;					98US-0083493P.
KW	prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.					98US-0083496P.
OS	Homo sapiens.					98US-0083559P.
XX						98US-0084414P.
XX						98US-0084639P.
XX						98US-0084640P.
XX						98US-0084643P.
XX						98US-0085579P.
XX						98US-0085580P.
XX						98US-0085582P.
XX						98US-0085700P.
XX						98US-0086023P.
XX						98US-0086392P.
XX						98US-0086486P.
XX						98US-0087098P.
XX						98US-0087208P.
XX						98US-0087609P.
XX						98US-0087753P.
XX						98US-0087827P.
XX						98US-0088025P.
XX						98US-0088028P.
XX						98US-0088029P.
XX						98US-0088031P.
XX						98US-0088328P.
XX						98US-0088167P.
XX						98US-0088202P.
XX						98US-0088212P.
XX						98US-0088217P.
XX						98US-0088555P.
XX						98US-0088722P.
XX						98US-0088738P.
XX						98US-0088740P.
XX						98US-0088811P.
XX						98US-0088824P.
XX						98US-0088825P.
XX						98US-0088828P.
XX						98US-0088861P.
XX						98US-0088863P.
XX						98US-0088876P.
XX						98US-0089090P.
XX						98US-0089105P.
XX						98US-0089512P.
XX						98US-0089514P.
XX						98US-0089538P.
XX						98US-0089598P.

Qy	781	ATGAAGTGTCTCAAAACCCGAGATGTGGCCGAGGCTGTATCTACGTCTCTAGACCCCCC	840	XX	21-JUN-2002;	2002US-00176756.	XX
Db	781	ATGAAGTGTCTCAAAACCCGAGATGTGGCCGAGGCTGTATCTACGTCTCTAGACCCCCC	840	XX	18-SEP-1997;	97US-0059263P.	XX
Qy	841	GCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCAGGTGACCTAGTGACTG	900	PR	17-OCT-1997;	97US-0062250P.	PR
Db	841	GCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCAGGTGACCTAGTGACTG	900	PR	21-OCT-1997;	97US-0063486P.	PR
Qy	901	TGGGAGCTCCTCTTCCCTCCCCACCCCTTCATGGCTTGCTCCTCTGCTCTGGATTTTAGG	960	PR	24-OCT-1997;	97US-0063120P.	PR
Db	901	TGGGAGCTCCTCTTCCCTCCCCACCCCTTCATGGCTTGCTCCTCTGCTCTGGATTTTAGG	960	PR	28-OCT-1997;	97US-0063540P.	PR
Qy	961	TGTTGATTTGGATACGGGATACACTTCTCTGTCACACCCGACAGGGGCTAGAAA	1020	PR	28-OCT-1997;	97US-0063544P.	PR
Db	961	TGTTGATTTGGATACGGGATACACTTCTCTGTCACACCCGACAGGGGCTAGAAA	1020	PR	29-OCT-1997;	97US-0063734P.	PR
Qy	1021	ATTTCGTTTGAGATTTTATATCATCTTGTCAAATTCCTTCAGTTGTAAATGTGAAAAATG	1080	PR	31-OCT-1997;	97US-0063870P.	PR
Db	1021	ATTTCGTTTGAGATTTTATATCATCTTGTCAAATTCCTTCAGTTGTAAATGTGAAAAATG	1080	PR	13-NOV-1997;	97US-0065311P.	PR
Qy	1081	GGCTGGGAAAGAGGTGTCCCTAATTTGTTTACTTGTGTTAACTTGTTCCTGTCGCC	1140	PR	21-NOV-1997;	97US-0066120P.	PR
Db	1081	GGCTGGGAAAGAGGTGTCCCTAATTTGTTTACTTGTGTTAACTTGTTCCTGTCGCC	1140	PR	24-NOV-1997;	97US-0066466P.	PR
Qy	1141	TGGGCACCTTGGCTTTGTCTGCTCTCAGTGTCTTCCCTTGACATGGGAAAGAGTTGTG	1200	PR	11-DEC-1997;	97US-0066772P.	PR
Db	1141	TGGGCACCTTGGCTTTGTCTGCTCTCAGTGTCTTCCCTTGACATGGGAAAGAGTTGTG	1200	PR	12-DEC-1997;	97US-0069425P.	PR
Qy	1201	GCCAAATCCCCATCTTCTTGACCTCAACGTCCTGTGGCTCAGGGCTGGGGTGGCAGAGG	1260	PR	18-DEC-1997;	97US-0068017P.	PR
Db	1201	GCCAAATCCCCATCTTCTTGACCTCAACGTCCTGTGGCTCAGGGCTGGGGTGGCAGAGG	1260	PR	10-MAR-1998;	98US-0077450P.	PR
Qy	1261	GAGGCCTTCACCTTATATCTGTGTATTCAGGGCTCCAGACTTCCTCTGCTGCTGC	1320	PR	11-MAR-1998;	98US-0077632P.	PR
Db	1261	GAGGCCTTCACCTTATATCTGTGTATTCAGGGCTCCAGACTTCCTCTGCTGCTGC	1320	PR	11-MAR-1998;	98US-0077649P.	PR
Qy	1321	CCCACTGACCTCTCCCTTATCTATCTCTCTCCGCTCCGAGCCAGTCTTGGCT	1380	PR	20-MAR-1998;	98US-0078886P.	PR
Db	1321	CCCACTGACCTCTCCCTTATCTATCTCTCTCCGCTCCGAGCCAGTCTTGGCT	1380	PR	27-MAR-1998;	98US-0078939P.	PR
Qy	1381	CTTTCTCCCTCCTCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACCA	1440	PR	31-MAR-1998;	98US-0080107P.	PR
Db	1381	CTTTCTCCCTCCTCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACCA	1440	PR	31-MAR-1998;	98US-0080194P.	PR
Qy	1441	GGGCTGGCCAGTGGATTTCATGTGATCATTAATAAGAAAAATCGCAACCAAAAAA	1500	PR	01-APR-1998;	98US-0080327P.	PR
Db	1441	GGGCTGGCCAGTGGATTTCATGTGATCATTAATAAGAAAAATCGCAACCAAAAAA	1500	PR	08-APR-1998;	98US-0081049P.	PR
Qy	1501	AAAAA 1505		PR	08-APR-1998;	98US-0081070P.	PR
Db	1501	AAAAA 1505		PR	09-APR-1998;	98US-0081195P.	PR
RESULT 6				PR	15-APR-1998;	98US-0081838P.	PR
ACA71168				PR	21-APR-1998;	98US-0082568P.	PR
ID ACA71168 standard; cdna; 1505 BP.				PR	21-APR-1998;	98US-0082569P.	PR
XX				PR	22-APR-1998;	98US-0082704P.	PR
AC ACA71168;				PR	28-APR-1998;	98US-0083322P.	PR
XX				PR	29-APR-1998;	98US-0083495P.	PR
XX				PR	29-APR-1998;	98US-0083496P.	PR
XX				PR	29-APR-1998;	98US-0083499P.	PR
XX				PR	05-MAY-1998;	98US-0083559P.	PR
XX				PR	06-MAY-1998;	98US-0084366P.	PR
XX				PR	07-MAY-1998;	98US-0084414P.	PR
XX				PR	07-MAY-1998;	98US-0084643P.	PR
XX				PR	15-MAY-1998;	98US-0085579P.	PR
XX				PR	15-MAY-1998;	98US-0085580P.	PR
XX				PR	15-MAY-1998;	98US-0085582P.	PR
XX				PR	15-MAY-1998;	98US-0085700P.	PR
XX				PR	18-MAY-1998;	98US-0086023P.	PR
XX				PR	22-MAY-1998;	98US-0086392P.	PR
XX				PR	28-MAY-1998;	98US-0086486P.	PR
XX				PR	28-MAY-1998;	98US-0087098P.	PR
XX				PR	02-JUN-1998;	98US-0087208P.	PR
XX				PR	02-JUN-1998;	98US-0087609P.	PR
XX				PR	03-JUN-1998;	98US-0087827P.	PR
XX				PR	04-JUN-1998;	98US-0088025P.	PR
XX				PR	04-JUN-1998;	98US-0088028P.	PR
XX				PR	04-JUN-1998;	98US-0088029P.	PR
XX				PR	04-JUN-1998;	98US-0088031P.	PR
XX				PR	04-JUN-1998;	98US-0088326P.	PR
XX				PR	05-JUN-1998;	98US-0088167P.	PR
XX				PR	05-JUN-1998;	98US-0088202P.	PR
XX				PR	05-JUN-1998;	98US-0088212P.	PR
PD							

Human secreted/transmembrane protein (PRO) cdna #189.
Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
tissue typing.
Homo sapiens.
US2003032112-A1.
13-FEB-2003.

Qy	481	GCCTCTAGCATCTGCA	CA	CGGAGACGCTTA	CCAGTTC	CAATGAAGGAGCGGAATGTGGACGAT	540		
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Qy	481	GCCTCTAGCATCTGCA	CA	CGGAGACGCTTA	CCAGTTC	CAATGAAGGAGCGGAATGTGGACGAT	540		
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Qy	541	GGGCACATCAATTAACAT	CA	ATAGATGCT	TGGCCACCGAGTGT	TACCCCTGTCTGTGACC	600		
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Qy	541	GGGCACATCAATTAACAT	CA	ATAGATGCT	TGGCCACCGAGTGT	TACCCCTGTCTGTGACC	600		
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Qy	601	CAC	TTCTATAGTGC	CA	CAAGTAGTCGCGT	CAC	TGCGCTGACAGAGGAC	TGAGCGCAAGAG	660
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Qy	601	CAC	TTCTATAGTGC	CA	CAAGTAGTCGCGT	CAC	TGCGCTGACAGAGGAC	TGAGCGCAAGAG	660
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Qy	661	CTTCGGGAGGCCAG	ACCA	CATCCGAGCCAC	CGTGC	ATCTCTCAGTGTGGTGGAGACA	720		
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Qy	661	CTTCGGGAGGCCAG	ACCA	CATCCGAGCCAC	CGTGC	ATCTCTCAGTGTGGTGGAGACA	720		
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Qy	721	CAATTCGCTTCAAACT	TCCAGCA	AGGACCCCTG	GAGAGG	CAGCTGC	CACTATGAGCAA	780	
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Qy	721	CAATTCGCTTCAAACT	TCCAGCA	AGGACCCCTG	GAGAGG	CAGCTGC	CACTATGAGCAA	780	
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Qy	781	ATGAAGTGTCTCAA	ACCCGAGGATGT	GGCCGAGGCTGT	TATCTAC	GTCTCAGCACCCCC	840		
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Qy	901	TGGGAGCTCCCT	TCCTCC	CCACCCCTCAT	TGGCTTC	CTCTGCTCTGGATTTT	TAGG	960	
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Qy	901	TGGGAGCTCCCT	TCCTCC	CCACCCCTCAT	TGGCTTC	CTCTGCTCTGGATTTT	TAGG	960	
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Qy	1081	GCCTGGGAAAGAG	GGTGGT	CTCC	TAATGTTTTA	CTTGTTAACT	TGTTCTTTGTGCCCC	1140	
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Qy	1321	CCCACTGC	AC	CCCTTATCT	ATCTCTT	CTCGGCTCC	CCAGCCCACTGTGGCT	1380	
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RESULT 7	
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XX	
DT	05-AUG-2003 (first entry)
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DE	Human secreted polypeptide PRO1774-encoding cDNA, SEQ ID NO:377.
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KW	Human; PRO; secreted protein; transmembrane protein;
KW	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW	chondrocyte; proliferation; differentiation; cartilage disorder;
KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW	liver; drug screening; transgenic animal; genetic analysis;
KW	antiarthritic; vulnereary; gene therapy; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	US2003027278-A1.
XX	
PD	06-FEB-2003.
XX	
PF	21-JUN-2002; 2002US-00176987.
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PR	18-SEP-1997; 97US-0059263P.
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PR	17-OCT-1997; 97US-0062250P.
PR	21-OCT-1997; 97US-0063486P.
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Query Match

Best Local Similarity

Matches 1505;

Score 1505;

DB 7;

Length 1505;

100.0%;

Pred. No. 0;

Conservative

Mismatches

0;

Indels

0;

Gaps

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RESULT 8
ACCS87082
ID ACC87082 standard; cDNA; 1505 BP.
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XX 05-AUG-2003 (first entry)
XX Human secreted polypeptide PRO1774-encoding cDNA, SEQ ID NO:377.
DE Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy; gene; ss.
XX Homo sapiens.
XX US2003036159-A1.
PN 20-FEB-2003.
PD 02-JUL-2002; 2002US-00188773.
PF 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
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QY	241	ACTGTGGGCAACATCGAGGAGTGGCTGCTGAATGTAAAGTGCAGGCTACCCGGGACT	300
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QY	541	GGGACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACC	600
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KW	chromosome mapping; gene mapping; cytostatic; gene therapy; gene; ss.		

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KW      chondrocyte differentiation; tumour necrosis factor-alpha release; ss;
KW      affinity purification; gene.
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OS      Homo sapiens.
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PN      US2003036147-A1.
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PD      20-FEB-2003.
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PF      02-JUL-2002; 2002US-00187741.
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PR	10-AUG-1998;	98US-0096012P.	Db	121	CCCGCATGGAGCGGTGGCGGACCGGCTGGCGTGTGACGGGGGCTCGGGGGGCATC	180
PR	17-AUG-1998;	98US-0096757P.				
PR	17-AUG-1998;	98US-0096766P.				
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PR	17-AUG-1998;	98US-0096891P.	Db	181	GGCGGGCGGTGGCCCGGGCCCTGGTCCAGCAGGGACTGAAAGTGGTGGGCTCGGCCCGC	240
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PR	18-AUG-1998;	98US-0097022P.	Db	241	ACTGTGGGCAACATCGAGGAGCTGGCTGCTGAATGTAAAGTGCAGGCTACCCGGGACT	300
PR	26-AUG-1998;	98US-0097952P.				
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PR	26-AUG-1998;	98US-0097971P.				
PR	26-AUG-1998;	98US-0097974P.	QY	361	ATCCGTTCTCAGCAGCGGTGTAGACATCTGATCAACAAATGCTGGCTTGGCCCGGCGCT	420
PR	01-SEP-1998;	98US-0098014P.	Db	361	ATCCGTTCTCAGCAGCGGTGTAGACATCTGATCAACAAATGCTGGCTTGGCCCGGCGCT	420
PR	01-SEP-1998;	98US-0098716P.				
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PR	02-SEP-1998;	98US-0098821P.				
PR	09-SEP-1998;	98US-0098843P.	QY	481	GCCCTCAGCATCTGCACACGGGAAGCTTACAGTCCATGAAGGAGCGGAATGTGGACGAT	540
PR	10-SEP-1998;	98US-0099602P.	Db	481	GCCCTCAGCATCTGCACACGGGAAGCTTACAGTCCATGAAGGAGCGGAATGTGGACGAT	540
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PR	10-SEP-1998;	98US-0099763P.	Db	541	GGGCACATCTTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACC	600
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PR	17-SEP-1998;	98US-0100684P.	Db	661	CTTCGGAGGCCAGACCCACATCCGAGCCACGTGCATCTCTCAGGTGTGGTGGAGACA	720
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PR	17-SEP-1998;	98US-0100930P.	QY	721	CAATTCGGCTTCAAACTCCAGCAAGGACCCCTCAGAAAGCAGCTGCACCTATGAGCAA	780
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PR	23-SEP-1998;	98US-0101471P.	Db	781	ATGAAGTGTCTCAAACCGGAGATGTGGCCGAGGCTGTATCTACGTCCTCAGACCCCC	840
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PR	23-SEP-1998;	98US-0101475P.	QY	841	GCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGAGGTGACTAGTGACTG	900
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Novel human secreted and transmembrane protein PRO1774 cDNA.

Human; secreted and transmembrane protein; PRO; transgenic animal;
knockout; chromosome identification; tissue typing; tumour;
chondrocyte proliferation; chondrocyte differentiation;
tumor necrosis factor-alpha release stimulator; gene; ss.

Homo sapiens.

US2003036144-A1.

20-FEB-2003.

01-JUL-2002; 2002US-00187601.

18-SEP-1997; 97US-0059263P.

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GenCore version 5.1.6
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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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VERSION AX092396.1 GI:13444512
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,K.K. and
Wood,W.I.

AX092396 1505 bp DNA linear PAT 21-MAR-2001

TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL	Patent: WO 0116318-A 127 08-MAR-2001; Genentech, Inc. (US)
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ABRAMSON,R.D., MULLAHY,S.J., BOSAK,S.A., MCEWAN,P.J., MCKERNAN,K.J., MALEK,J.A., GUNARATNE,P.H., RICHARDS,S., WORLEY,K.C., HALE,S., GARCIA,A.M., GAY,L.J., HULYK,S.W., VILLALON,D.K., MUZNY,D.M., SODERGREN,E.J., LU,X., GIBBS,R.A., FAHEY,J., KELTON,E., KETTEMAN,M., MADAN,A., RODRIGUES,S., SANCHEZ,A., WHITING,M., MADAN,A., YOUNG,A.C., SHEVCHENKO,Y., BOUFFARD,G.G., BLAKESLEY,R.W., TOUCHMAN,J.W., GREEN,E.D., DICKSON,M.C., RODRIGUES,A.C., GRIMWOOD,J., SCHMUTZ,J., MYERS,R.M., BUTTERFIELD,Y.S., KRZYWIŃSKI,M.I., SKALAKA,U., SMALLUS,D.E., SCHNERCH,A., SCHEIN,J.E., JONES,S.J. and MARRA,M.A.	23388257	12477932	2 (bases 1 to 1501)	Strausberg,R. Direct Submission	Submitted (05-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	NTH-MGC Project URL: http://mgc.nci.nih.gov On Aug 19, 2003 this sequence version replaced gi:12803782. Contact: MGC help desk Email: cgabbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@hgrl.nih.gov Akhter N., Ayèle,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Iaric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Turgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
CLONE DISTRIBUTION: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 12 Row: g Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13236541 Location/Qualifiers 1. .1501 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:4172 IMAGE:3631177" /tissue_type="uterus, endometrium adenocarcinoma" /clone_lib="NIH_MGC_44" /lab_host="DH10B-R" /note="vector: pOTB7" 1. .1501 /gene="MGC4172" /note="synonym: FLJ22543" /db_xref="LocusID:79154" 338..883 /codon_start=1 /product="hypothetical protein MGC4172" /protein_id="AAH02731.1" /db_xref="GI:12803783" /db_xref="LocusID:79154" /translation="MFSAIRSQHSQVDICINNAGLRPDTLLSGSTSGWKDMFNVNVI ALSICREAYQSKMRNVDDGHIININMSGRVLPISVTHFYSAKYAVTALTEGLR QELREAGTHIRATCISPGVVEVTFQAFKLHDKDPEKAAATYQMCKLPEDVAEAVIY LSTPAHFIGIDIQMRPTEQVT" 338..832						
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ACCESSION AK026196
VERSION AK026196.1 GI:10438967
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1
AUTHORS Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,
Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1410)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail: flicdn@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).

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ACCESSION AX834229
VERSION AX834229.1 GI:39920364
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
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ACCESSION	ACLI0594		
VERSION	ACLI0594.5	GI:22830329	
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ORGANISM	Homo sapiens		
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Birren,B., Nusbaum,C. and Lander,E.		
JOURNAL	Homo sapiens chromosome 17, clone CTD-2193J24		
REFERENCE	Unpublished		
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campiano,A., Chang,J., Chazarov,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Govettte,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamae,A., Karatas,A., Kells,C., Lakocue,K., Lamazares,R., Landers,T., Lenockzy,J., Levine,R., Liu,G., MacLean,C., MacDonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severly,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye-W.J., Young,G., Zainoun,J., Zembeke,L., Zimmer,A. and Zody,M.		
Direct Submission			
TITLE	Submitted (13-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
JOURNAL	Research		
REFERENCE	3 (bases 1 to 159490)		
AUTHORS	Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazarov,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamae,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., MacDonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severly,P.,		

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RESULT 11
AX768992 2077 bp DNA linear PAT 02-JUL-2003
LOCUS Sequence 109 from Patent WO02098917.
DEFINITION AX768992
ACCESSION AX768992
VERSION AX768992.1 GI:32437160
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Guo, X., Fernandes, E., Li, L., Kekuda, R., Liu, Y., Leite, M., Spytek, K.A., Ji, W., Casman, S.J., Boldog, F.L., Patturajan, M., Vernet, C.A., Ballinger, R.A., Malyankar, U.M., Tchernev, V.T., Blalock, A.D., Gusev, V.Y., Rastelli, L., Mezes, P.D., Ellerman, K., Heyes, M., Herrmann, J.L., Shimkets, R.A., Ioime, N., Pena, C.E., Shenoy, S.G., Taupier, R.J., Gerlach, V. and Gorman, L.
TITLE Human proteins and nucleic acids encoding same
JOURNAL Patent: WO 02098917-A 109 12-DEC-2002;
FEATURES Curagen Corporation (US)
location/Qualifiers
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source
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QY	547 ATCATTTAATCATATAGCATGTCTGGCCACCGAGTGTACCCCTGCTGTGACCCACTTC 606				
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DB	541 GAGCCCGACACCCACATCCGAGCCACGTG 569				
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LOCUS	Sequence 89 from patent US 6342581.				
DEFINITION	AR184145				
ACCESSION	AR184145.1	GI:20228114			
VERSION					
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 569)				
AUTHORS	Rosen,C.A., Ruben,S.M., Olsen,H.S. and Ebner,R.				
TITLE	Secreted protein HUHP03				
JOURNAL	Patent: US 6342581-A 89 29-JAN-2002;				
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KYAW,
PI YI LI, ZHIZHEN ZENG, DAVID W LAFLEUR, PAUL A MOORE, YANGGU SHI, PI
HENRIK S OLSEN,
PI REINHARD EBNER, LAURIE A BREWER
PC C07H21/04, C12N15/63
CC n equals a,t,g, or c
FH Key Location/Qualifiers
FT misc feature (1).
Location/Qualifiers
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FEATURES

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ORIGIN

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102 TTCAGTCTAAATGTGAAAATGGGCTGGGGAAGGAGGTGTGCCCTAATTGTTTAC 161
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Db |||||
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RESULT 14

AX330105/c

LOCUS AX330105 430 bp DNA linear PAT 09-JAN-2002

DEFINITION Sequence 614 from Patent WO0194629.

ACCESSION AX330105

VERSION AX330105.1 GI:18103083

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,

Horrigan, S., Soppet, D.R. and Weaver, Z.

Cancer gene determination and therapeutic screening using signature

gene sets

Patent: WO 0194629-A 614 13-DEC-2001;

Avalon Pharmaceuticals (US)

Location/Qualifiers

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source

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ORIGIN

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Matches 428; Conservative 0; Mismatches 0;
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Db |||||
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RESULT 15

AC015919/c

LOCUS AC015919 169713 bp DNA linear HTG 13-JUL-2000

DEFINITION Homo sapiens chromosome 17 clone CTD-2047D24 map 17, LOW-PASS

SEQUENCE SAMPLING.

ACCESSION AC015919

VERSION AC015919.2 GI:9176716

KEYWORDS HTG; HTGS PHASE0.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 169713)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 17, clone CTD-2047D24

Unpublished

2 (bases 1 to 169713)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

Baldwin, J., Barna, N., Becker, R., Boguslavsky, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArelano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,

Gallagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,

McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,

Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Direct Submission

TITLE

JOURNAL

COMMENT

Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jul 13, 2000 this sequence version replaced gi:6446748.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L855
 Center clone name: 2047_D_24

* NOTE: This record contains 177 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 60.0 , Gapext 60.0

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22: em_gss_man:**
23: em_gss_mus:**
24: em_gss_pro:**
25: em_gss_rod:**
26: em_gss_phg:**
27: em_gss_vrl:**
28: gb_gss1:**
29: gb_gss2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	654	43.5	1071	13	BQ278156
					BQ278156 AGENCOURT

5	627	41.7	627	12	BM848012
6	624	41.5	822	12	BG741589
7	609	40.5	640	12	BM755987
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9	602	40.0	602	12	BM764342
10	586	38.9	1022	9	AL559036
11	583	38.7	649	12	BM717452
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13	576	38.3	672	13	BU624717
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15	573	38.1	573	12	BM742038
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17	543	36.1	932	10	EG030249
18	541	35.9	541	12	BG231973
19	531	35.3	582	12	BM737591
20	523	34.8	651	9	AV654573
21	516	34.3	540	12	BM848396
22	515	34.2	572	12	BM682228
23	511	34.0	550	12	BM743569
24	496	33.0	769	10	BE386240
25	489	32.5	489	9	AI125225
26	488	32.5	566	14	CA424831
27	488	32.4	658	12	BM723373
28	477	31.7	513	10	BE302814
29	470	31.2	479	9	AN050614
30	469	31.2	570	12	BM675954
31	457	30.4	691	12	BM739299
32	455	30.2	455	10	BE395404
33	453	30.1	516	12	BM708058
34	451	30.0	886	10	BE895089
35	441	29.3	481	9	AI673434
36	438	29.1	476	9	AI803690
37	437	29.0	474	12	BM712008
38	435	28.9	435	9	AI129923
39	433	28.8	804	12	BI765897
40	428	28.4	430	9	AA448177
41	427	28.4	669	14	CB851997
42	425	28.2	1063	10	BE796469
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44	423	28.1	614	10	BE869917
45	418	27.8	550	10	BE931725
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47	417	27.7	757	12	BI464353
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50	405	26.9	456	9	AI378033
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54	387	25.7	489	12	BG717600
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56	371	24.7	408	9	AA809706
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61	355	23.6	385	12	BM681153
62	349	23.2	376	12	BM717586
63	346	23.0	546	12	BI260323
64	345	22.9	398	9	AI200014
65	342	22.7	645	13	B0731451
66	339	22.5	388	12	BQ011157
67	338	22.5	538	13	BI111640
68	332	22.1	852	12	BG282361
69	308	20.5	480	10	AW131630
70	307	20.4	354	12	BM727723
71	306	20.3	363	9	AA877467
72	286	19.0	351	10	BE173801
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74	276	18.3	787	10	BF967768
75	274	18.2	458	10	BE857374
76	271	18.0	714	12	BI546418
77	265	17.6	389	10	AW371789

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BM755987 K-EST0034
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BM764342 K-EST0045
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BM717452 UI-E-EJO-
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BU624717 UI-H-FGI-
BU539642 AGENCOURT
BM742038 K-EST0014
BM744024 K-EST0017
EG030249 602297547
BG231973 nat34g12.
BM737591 K-EST0000
AV654573 AV654573
BM848396 K-EST0128
BM682228 UI-E-EJO-
BM743569 K-EST0016
BE386240 601273447
AI125225 qd87f01.x
CA424831 UI-H-PEI-
BM723373 UI-E-EJO-
BE302814 ba69c04.Y
AW050614 wz19c10.x
BM675954 UI-E-EJO-
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BE395404 601309913
BM708058 UI-E-CL1-
BE895089 601436007
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AI803690 tc19e02.x
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BI765897 603046146
AA448177 zw83d12.s
CB851997 UI-CF-FN0
BE796469 601589817
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BE931725 QV4-HT053
EG037061 602288368
BI464353 603204005
AL568188 AL568188
AW050632 wz19e08.x
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AW974208 EST386311
AL559035 AL559035
AI620164 tu46c12.x
BG717600 602698216
AW001572 wu34f05.x
AA809706 nk96f06.s
AI221658 qg93d04.x
BM674861 UI-E-EJO-
EG983161 IL5-CN006
AI214596 qm28h07.x
BM681153 UI-E-EJO-
BM717586 UI-E-EJO-
BI260323 602969342
AI200014 qf90d03.x
B0731451 UI-E-CIL-
BQ011157 UI-1-BC1p
BI111640 BX111640
BG282361 602402863
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BM727723 UI-E-EJO-
AA877467 ob33h03.s
BE173801 CM0-HT056
AI422493 tf11d03.x
BF967768 602287657
BE857374 7937h03.x
BI546418 603188719
AW371789 CM2-BT030

C 78	263	17.5	376	14	T49180	T49180 yb09h06.r1
C 79	254	16.9	486	9	AA308673	AA908673 o10ad06.s
C 80	254	16.9	535	14	W58347	W58347 zd25b06.s1
C 81	253	16.8	413	9	AA575928	AA575928 nm56b12.s
C 82	252	16.7	312	13	BA480776	BA480776 DKFZp686C
C 83	249	16.5	352	10	BF375427	BF375427 MR4-ST024
C 84	249	16.5	374	10	AW392371	AW392371 MR4-ST024
C 85	248	16.5	539	12	BG488598	BG488598 602534511
C 86	246	16.3	299	10	AW351512	AW351512 IL2-CT003
C 87	246	16.3	641	13	BA488597	BA488597 DKFZp686L
C 88	246	16.3	748	12	BI761329	BI761329 603044093
C 89	237	15.7	417	10	AW371786	AW371786 CM2-BT030
C 90	234	15.5	242	9	AI699226	AI699226 tx62e11.x
C 91	234	15.5	1171	12	BM800956	BM800956 AGENCOURT
C 92	229	15.2	511	9	AI356759	AI356759 qy22f10.x
C 93	228	15.1	940	12	BI818880	BI818880 603037354
C 94	220	14.6	651	9	AA717295	AA717295 AV7132795
C 95	214	14.2	348	9	AA723851	AA723851 ah63406.s
C 96	214	14.2	395	10	AW371791	AW371791 CM2-BT030
C 97	210	14.0	333	14	D60924	D60924 HUM139B12B
C 98	205	13.6	567	14	W58472	W58472 zd25b06.r1
C 99	204	13.6	536	14	W58459	W58459 zd25b06.s1
C 100	201	13.4	465	12	BM825434	BM825434 K-EST0097

ALIGNMENTS

RESULT 1	829 bp	linear	EST 27-FEB-2001
BG324477		mrna	
LOCUS	6024242421F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4560485 5',		
DEFINITION	RNA sequence.		
ACCESSION	BG324477		
VERSION	BG324477.1		
KEYWORDS	GI:13130914		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	1. (bases 1 to 829)		
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: DCTD/BTP CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCMI269 row: j column: 06 High quality sequence stop: 755.		

FEATURES	SOURCE
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RESULT 2
BM471232

LOCUS	ACCESSION
DEFINITION	VERSION
	KEYWORDS
	SOURCE
	ORGANISM

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1				
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Query Match	44.9%;	Score 675;	DB 12;	Length 829;		
Best Local Similarity	100.0%;	Pred. No. 4.1e-219;	Indels	0;		
Matches 675;	Conservative	0;	Mismatches	0;		
45	GC	CGGCGTCA	CTCTCG	ACCCCGTGTCTCGAGCGGTAGTCCACGAGGCGGACGGCGGCG 104		
b						
1	GC	CGGCGTCA	CTCTCG	ACCCCGTGTCTCGAGCGGTAGTCCACGAGGCGGACGGCGGCG 60		
105	TG	GGCCCATG	GGCCAG	GGCCGGCATGAGCGGTGGCGCGACCGGCTGGCGCTGGTGA		
Y						
b						
61	TG	GGCCCATG	GGCCAG	GGCCGGCATGAGCGGTGGCGCGACCGGCTGGCGCTGGTGA		
Y						
165	GG	CTTCGG	GGGGAT	TCGGCGGGCGTGGCCCGGGCCCTGGTCCAGCAGGACTGAAGT 224		
Y						
b						
121	GG	CTTCGG	GGGGAT	TCGGCGGGCGTGGCCCGGGCCCTGGTCCAGCAGGACTGAAGT 180		
Y						
b						
225	GT	TGGGCT	CGCCCG	CACCTG	GGGCAACATCAGAGAGCTGGCTGCTGTAATGTAAGAGTGC 284	
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b						
181	GT	TGGGCT	CGCCCG	CACCTG	GGGCAACATCAGAGAGCTGGCTGCTGTAATGTAAGAGTGC 240	
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b						
285	AG	GCTAC	CCCGG	ACTTTG	ATCCCTTACAGATGTGACCTTACAAATGAAGAGACATCCT 344	
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b						
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301	CT	CCATG	TTCTC	AGCTAT	CGTTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGC 360	
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b						
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525	GC	GAATGT	GGACGA	TATCA	TATTAA	CATCAATAGCATGTCTGGCCACCGAGTGT 584
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541	AC	CCCTGT	CTGTG	ACCCAC	CTTCTAT	AGTGGCCACAAAGTATGCCGTCACTGCGCTGCACGA 600
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b						
601	GG	GACTG	GAGCA	AGATT	TCGGAGG	CCCAACATCCGAGCCACGTGCAATCTCTCC 660
Y						
b						
705	AG	TGTG	GTGG	AGAC	719	
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661	AG	TGTG	GTGG	AGAC	675	
Y						
b						

BM471232	1010 bp	linear	EST 05-FEB-2002
LOCUS	AGSNCOURT_6478395	NIH_MGC_72	Homo sapiens cDNA clone IMAGE:5563124
DEFINITION	5', mRNA sequence.		
ACCESSION	BM471232		
VERSION	BM471232.1	GI:18520274	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1010)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC/DCTD/DTP		

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12293 row: j column: 21
 High quality sequence stop: 561.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:5563124"
 /tissue_type="melanotic melanoma"
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 /clone_lib="NIH_MGC_72"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

ORIGIN

Query Match 44.4%; Score 668; DB 12; Length 1010;
 Best Local Similarity 100.0%; Pred. No. 8.9e-217;
 Matches 668; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 15 GAGCGGCGGCGCTCAGCTCTCGACCCCGCTGTGCGGCTAGTCAGGAGCGGACGGG 74
 QY 100 CGGCGTGGGCGCCATGCGGCGGCGGATGAGCGGTGGCGCGGCGGCGGCTGGTG 159
 Db 75 CGGCGTGGGCGCCATGCGGCGGCGGATGAGCGGTGGCGCGGCGGCGGCTGGTG 134
 QY 160 ACGGGGCGCTCGGGGGGATCGGCGCGGCGGCTGTGCGGCGGCGGCGGCGGCGG 219
 Db 135 ACGGGGCGCTCGGGGGGATCGGCGCGGCGGCTGTGCGGCGGCGGCGGCGGCGG 194
 QY 220 AAGTGTGTGGCTCGGCGGCGGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 279
 Db 195 AAGTGTGTGGCTCGGCGGCGGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 254
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 Db 255 AGTCAGGCTACCCCGGCGGCTTTGATCCCTACAGATGTGACCTATCAATGAAGAGAC 314
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 Db 555 GTGTTACCCCTGTCTGACCCACTTCTATAGTGCACCAAGTATGCGGCTCAGTGGCTG 614
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 QY 700 TCTCCAGG 707
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Db

675 TCTCCAGG 682

RESULT 3

BF979853/c

LOCUS

DEFINITION

BF979853

ACCESSION

BF979853

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

679 bp mRNA linear EST 23-JAN-2001
 602288368T1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4374184 3',
 mRNA sequence.
 BF979853
 BF979853.1 GI:12347068
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 679)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10037 row: g column: 17
 High quality sequence start: 24
 High quality sequence stop: 679.
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 /db_xref="taxon:9606"
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 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
 (gctgag); Oligo-dr primed using primer
 5'-TTTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.2 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: this is
 a NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match 43.8%; Score 659; DB 10; Length 679;
 Best Local Similarity 100.0%; Pred. No. 1.2e-213;
 Matches 659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 679 CACCTATGAGCAAAATGAAGTGTCTCAAAACCCGAGGATGTGGCGAGGCTGTATCTACG 620
 QY 827 TCCTCAGACCCCGGACACATCCAGATTGGAGACATCCAGATGAGGCCCGACGAGGAGG 886
 Db 619 TCCTCAGACCCCGGACACATCCAGATTGGAGACATCCAGATGAGGCCCGACGAGGAGG 560
 QY 887 TGACCTAGTACGTGGGAGCTCCTCTCCCTCCCTCCCTCATGGCTGCTCCTCTGC 946
 Db 559 TGACCTAGTACGTGGGAGCTCCTCTCCCTCCCTCCCTCATGGCTGCTCCTCTGC 500
 QY 947 CTCTGATTTTGGTGTGATTTCTGGATCAGGGATACCACTTCTCTGTCCACACCCCGA 1006
 Db 499 CTCTGATTTTGGTGTGATTTCTGGATCAGGGATACCACTTCTCTGTCCACACCCCGA 440
 QY 1007 CCAGGGGCTAGAAAATTTGTTGAGATTTTATATCATCTTGTCAAATTCGTTCTGT 1066
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ORIGIN

BM848012 627 bp mRNA linear EST 06-MAR-2000
 K-EST0127637 S13KMS5 Homo sapiens cdna S13KMS5-43-A10 5',
 mRNA sequence.
 BM848012
 BM848012.1 GI:19204411
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 627)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korea EST Project 2001
 Unpublished (2002)
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 25 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel.: +82-42-860-4470

Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 43 row: A column: 10
 High quality sequence stop: 627.

FEATURES

source
 1..627
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 /note="Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP). The decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI which site is treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Beig method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 41.7%; Score 627; DB 12; Length 627;
 Best Local Similarity 100.0%; Pred. No. 9.2e-203;
 Matches 627; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AAGCAGTTCGCGCGCGGCGGAGAGAGCGCGCGCGTCTCAGCTCGACCCCGTGTG 74
 DB 1 AAGCAGTTCGCGCGCGGCGGAGAGAGCGCGCGTCTCAGCTCGACCCCGTGTG 60
 QY 75 GGGTAGTTCAGAGGCGGAGCGGCGCGGTGGGCCATGCCAGCCCGCATGGAGCG 134
 DB 61 GGGTAGTTCAGAGGCGGAGCGGCGCGGTGGGCCATGCCAGCCCGCATGGAGCG 120
 QY 135 GTGCGCGACCGGTGGCGGTGTCAGCGGGGCGTTCGGGGGCGATCGCGCGCGCGTGGC 194
 DB 121 GTGCGCGACCGGTGGCGGTGTCAGCGGGGCGTTCGGGGGCGATCGCGCGCGCGTGGC 180
 QY 195 CCGGGCCCTGTCCAGCAGGAGCTCAAGGTGGTGGGCTGCGCGCGCACTGTGGGCAACAT 254
 DB 181 CCGGGCCCTGTTCAGCAGGAGCTCAAGGTGGTGGGCTGCGCGCGCACTGTGGGCAACAT 240
 QY 255 CGAGGAGTGGTCTGAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 314
 DB 241 CGAGGAGTGGTCTGAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300
 QY 315 ATGTGACCTATCAATGAAGAGGACATCTCTCCATGTTCCTCAGCTATCCGTTCTCAGCA 374
 DB 301 ATGTGACCTATCAATGAAGAGGACATCTCTCCATGTTCCTCAGCTATCCGTTCTCAGCA 360
 QY 375 CAGCGGTGTAGACATCTGCATCAACATGTGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 434
 DB 361 CAGCGGTGTAGACATCTGCATCAACATGTGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 420
 QY 435 AGGCAGCACAGTGGTGGAGGACATGTTCAATGTGAACGTGTGGCCCTCAGCATCTG 494
 DB 421 AGGCAGCACAGTGGTGGAGGACATGTTCAATGTGAACGTGTGGCCCTCAGCATCTG 480
 QY 495 CACACGGGAAGCCTACCAAGTCCATGAAGGAGCGGAATGTGGACATGGGCACATCAATAA 554
 DB 481 CACACGGGAAGCCTACCAAGTCCATGAAGGAGCGGAATGTGGACATGGGCACATCAATAA 540
 QY 555 CATCAATAGCATGTCTGGCCACCAGGTGTTACCCCTGTCTGTGACCCACTTCTATAGTGC 614

DB 541 CATCAATAGCATGTCTGGCCACCAGTGTACCCCTGTGTGACCCACTTCTATAGTGC 600
 QY 615 CACCAAGTATGCGTCACTGCGCTGAC 641
 DB 601 CACCAAGTATGCGTCACTGCGCTGAC 627

RESULT 6

BG741589 822 bp mRNA linear EST 15-MAY-2001
 LOCUS 602635416F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4780659 5',
 DEFINITION mRNA sequence.
 ACCESSION BG741589
 VERSION BG741589.1 GI:14052242
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LHAM10639 row: p column: 04

High quality sequence stop: 803.

FEATURES

source
 1..822
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4780659"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Skn3"
 /note="Organ: skin; Vector: pCMV-SPORE6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 41.5%; Score 624; DB 12; Length 822;
 Best Local Similarity 100.0%; Pred. No. 8.5e-202;
 Matches 624; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 GTGGGCGCATGCGCGCGCGCGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 163
 DB 94 GTGGGCGCATGCG 153
 QY 164 GGGCGTGGGGGGCGCATCG 223
 DB 154 GGGCGTGGGGGGCGCATCG 213
 QY 224 TGTGGGCTGCG 283
 DB 214 TGTGGGCTGCG 273
 QY 284 CAGGCTACCG 343
 DB 274 CAGGCTACCG 333
 QY 344 TCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATG 403
 DB 334 TCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATG 393

404 CTGGCTTGGCCGCGCTGACACCCCTGCTCTCAGCAGCAGCAGTGGTGGAGACATGT 463
 394 CTGGCTTGGCCGCGCTGACACCCCTGCTCTCAGCAGCAGCAGTGGTGGAGACATGT 453
 464 TCAATGTGAAGTGTGCGCCCTCAGCATCTGCACACGGGAAGCCTACAGTCCATGAAGG 523
 454 TCAATGTGAAGTGTGCGCCCTCAGCATCTGCACACGGGAAGCCTACAGTCCATGAAGG 513
 524 AGCGGAATGTGGACGATGGGACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGT 583
 514 AGCGGAATGTGGACGATGGGACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGT 573
 584 TACCCCTGTCTGTGACCCACTTCTATAGTGCACCAAGTATGCCGTGCTGACAG 643
 574 TACCCCTGTCTGTGACCCACTTCTATAGTGCACCAAGTATGCCGTGCTGACAG 633
 644 AGGACTCAGCAAGAGCTTGGGAGGCCAGACCCACATCCGAGCCACGTGCTATCTCTC 703
 634 AGGACTCAGCAAGAGCTTGGGAGGCCAGACCCACATCCGAGCCACGTGCTATCTCTC 693
 704 CAGGTGTGGTGGAGACAAATTCG 727
 694 CAGGTGTGGTGGAGACAAATTCG 717

RESULT 7
 BM755987
 LOCUS
 DEFINITION K-EST0034121 S1SNUS Homo sapiens cDNA clone S1SNUS-38-A10 5', mRNA
 sequence.
 ACCESSION BM755987.1 GI:19085602
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 640)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 38 row: A column: 10
 High quality sequence stop: 640.

FEATURES
 Location/Qualifiers
 1..640
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S1SNUS-38-A10"
 /sex="F"
 /tissue_type="Aescites"
 /cell_type="Lymphoblast-like"
 /cell_line="SNU-5"
 /lab_host="top10F"
 /clone_lib="S1SNUS"
 /note="Organ: Stomach; Vector: pCNS; Site:1: EcoRI;
 Site:2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was

ORIGIN
 Query Match 40.5%; Score 609; DB 12; Length 640;
 Best Local Similarity 100.0%; Pred. No. 1.2e-196;
 Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 350 TGTCTCAGCTATCCGTTCTCAGCAGCAGCGGTAGACATCTGCATCAACATGTGGCT 409
 Db 1 TGTCTCAGCTATCCGTTCTCAGCAGCAGCGGTAGACATCTGCATCAACATGTGGCT 60
 QY 410 TGGCCCGGCTGACACCCCTGCTCTCAGCAGCAGCAGTGGTGGAGACATGTCAATG 469
 Db 61 TGGCCCGGCTGACACCCCTGCTCTCAGCAGCAGCAGTGGTGGAGACATGTCAATG 120
 QY 470 TGAAGTGTCTGGCCCTCAGCATCTGCACACGGGAAGCCTACAGTCCATGAGGAGCGGA 529
 Db 121 TGAAGTGTCTGGCCCTCAGCATCTGCACACGGGAAGCCTACAGTCCATGAGGAGCGGA 180
 QY 530 ATGTGGACGATGGGACATCAATTAACATCAATAGCATCTTGGCCACCGAGTGTACCCC 589
 Db 181 ATGTGGACGATGGGACATCAATTAACATCAATAGCATCTTGGCCACCGAGTGTACCCC 240
 QY 590 TGTCTGTGACCCACTTCTATAGTGCACCAAGTATGCCGTCACTCGCTGACAGAGGAC 649
 Db 241 TGTCTGTGACCCACTTCTATAGTGCACCAAGTATGCCGTCACTCGCTGACAGAGGAC 300
 QY 650 TGAGCAAGAGCTTCCGGAGGCCAGACCCACATCCGAGCCACGTGCTCTCCAGGTG 709
 Db 301 TGAGCAAGAGCTTCCGGAGGCCAGACCCACATCCGAGCCACGTGCTCTCCAGGTG 360
 QY 710 TGGTGGAGACACAATTCGCTTCAAACTCCACGACCAAGGACCCCTGAGAGGAGGTGCA 769
 Db 361 TGGTGGAGACACAATTCGCTTCAAACTCCACGACCAAGGACCCCTGAGAGGAGGTGCA 420
 QY 770 CCTATGAGCAAAATGAAGTGTCTCAAAACCGAGGATGTGCCGAGGCTGTATCTACGTCC 829
 Db 421 CCTATGAGCAAAATGAAGTGTCTCAAAACCGAGGATGTGCCGAGGCTGTATCTACGTCC 480
 QY 830 TCAGACACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACGAGGAGGTGA 889
 Db 481 TCAGACACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACGAGGAGGTGA 540
 QY 890 CCTAGTGAATGTGGGAGCTCTCTTCCCTCCACCCCTTCATGGCTTGCCTTCCTCCTC 949
 Db 541 CCTAGTGAATGTGGGAGCTCTCTTCCCTCCACCCCTTCATGGCTTGCCTTCCTCCTC 600
 QY 950 TGGATTTTA 958
 Db 601 TGGATTTTA 609

RESULT 8
 BE617298
 LOCUS
 DEFINITION 601441804F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846168 5',
 mRNA sequence.
 ACCESSION BE617298
 VERSION BE617298.1 GI:9888236
 KEYWORDS
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 923)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLAM9558 row: 9 column: 01
High quality sequence stop: 698.

FEATURES
source

1..923
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3846168"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 65"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.8 Kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 40.1%; Score 603; DB 10; Length 923;
Best Local Similarity 100.0%; Pred. No. 1.1e-194;
Matches 603; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 332 AAGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCAGCGGTGAGACATCT 391
Db 1 AAGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCAGCGGTGAGACATCT 60

QY 392 GCATCAACAATCTGGCTTGGCCCGGCTGACACCTGCTCTCAGGAGCAGCAGTGGTT 451
Db 61 GCATCAACAATCTGGCTTGGCCCGGCTGACACCTGCTCTCAGGAGCAGCAGTGGTT 120

QY 452 GGAGGAGCATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACGGGAGCCTACC 511
Db 121 GGAGGAGCATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACGGGAGCCTACC 180

QY 512 AGTCCATGAGGAGCGGAATGTGACGATGGCAGCATCAATTAATCAATAGCATGTCTG 571
Db 181 AGTCCATGAGGAGCGGAATGTGACGATGGCAGCATCAATTAATCAATAGCATGTCTG 240

QY 572 GCCACCGAGTGTACCCCTGTTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCA 631
Db 241 GCCACCGAGTGTACCCCTGTTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCA 300

QY 632 CTGCGCTGACAGAGGAGTGAAGCAAGAGCTTCGGGAGGCCAGCAGCCAGATCCGAGCCA 691
Db 301 CTGCGCTGACAGAGGAGTGAAGCAAGAGCTTCGGGAGGCCAGCAGCCAGATCCGAGCCA 360

QY 692 CGTGCAATCTCTCCAGGTGTGGTGAGACACAATTCGCTTCAAACTCCAGCAGAGGACC 751
Db 361 CGTGCAATCTCTCCAGGTGTGGTGAGACACAATTCGCTTCAAACTCCAGCAGAGGACC 420

QY 752 CTGAGAGGAGCGTGCACCTATGAGCAATGAAGTGTCTCAAACTCCAGGAGTGTGGCGG 811
Db 421 CTGAGAGGAGCGTGCACCTATGAGCAATGAAGTGTCTCAAACTCCAGGAGTGTGGCGG 480

QY 812 AGGCTGTATCTAGTCTCTCAGCAGCCCGCCAGACATCCAGATGGAGATCCAGATGA 871
Db 481 AGGCTGTATCTAGTCTCTCAGCAGCCCGCCAGACATCCAGATGGAGATCCAGATGA 540

QY 872 GGCCACGAGGAGGTGACCTAGTGTGAGGAGTCTCTCTTCCCTCCCGACCCCTTCA 931
Db 541 GGCCACGAGGAGGTGACCTAGTGTGAGGAGTCTCTCTTCCCTCCCGACCCCTTCA 600

QY 932 TGG 934
|||

Db

601 TGG 603

RESULT 9

BM764342

LOCUS

DEFINITION

BM764342 602 bp mRNA linear EST 04-MAR-2002
X-EST0045842 S1SNUS Homo sapiens cDNA clone S1SNUS-39-A06 5', mRNA
sequence.

ACCESSION

BM764342

VERSION

BM764342.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 602)

AUTHORS

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

TITLE

21C Frontier Korean EST Project 2001

JOURNAL

Unpublished (2002)

COMMENT

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 39 row: A column: 06

High quality sequence stop: 602.

Location/Qualifiers

1..602

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S1SNUS-39-A06"

/sex="F"

/tissue_type="Ascites"

/cell_line="Lymphoblast-like"

/lab_host="Top10P"

/clone_lib="S1SNUS"

/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10P by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."FEATURES
source

ORIGIN

Query Match 40.0%; Score 602; DB 12; Length 602;
Best Local Similarity 100.0%; Pred. No. 2.9e-194;
Matches 602; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 TGTTCACGATATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGCT 409
Db 1 TGTTCACGATATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGCT 60

QY 410 TGGCCCGGGCTGACACCCCTGCTCTCAGGAGCAGCAGTGTGTGGAAGGACATGTTCAATG 469
Db 61 TGGCCCGGGCTGACACCCCTGCTCTCAGGAGCAGCAGTGTGTGGAAGGACATGTTCAATG 120

QY 470 TGAACGTGTGGCCCTCAGCATCTGCACACGGGAGCCTACCAGTCCATGAAGGAGCGGA 529
|||

Db

121

TGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCTTACAGTCCATGAAGAGCGGA

180

Qy

530

ATGTGGACAGTGGGACACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCC

589

Db

181

ATGTGGACAGTGGGACACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCC

240

Qy

590

TGCTGTGACCACTTCTATAGTCCCAAGTATGCCGTCACTGCGCTGACAGGGAC

649

Db

241

TGCTGTGACCACTTCTATAGTCCCAAGTATGCCGTCACTGCGCTGACAGGGAC

300

Qy

650

TGAGCAAGACTTGGGAGGCCACACCCACATCCGAGCCACGTGCACTCTCCAGTG

709

Db

301

TGAGCAAGACTTGGGAGGCCACACCCACATCCGAGCCACGTGCACTCTCCAGTG

360

Qy

710

TGGTGGAGACAAATTCGCCCTTCAAATCCACGACCAAGGACCTTGAGAAGGCAGCTGCCA

769

Db

361

TGGTGGAGACAAATTCGCCCTTCAAATCCACGACCAAGGACCTTGAGAAGGCAGCTGCCA

420

Qy

770

CCTATGACAAATGAAGTGTCTCAAAACCGAGGATGTGGCCGAGCTGTATCTACGTCC

829

Db

421

CCTATGACAAATGAAGTGTCTCAAAACCGAGGATGTGGCCGAGCTGTATCTACGTCC

480

Qy

830

TCAGACACCCCGCACATCCAGATTGGAGACATCCAGATGAGGCCACGAGGAGTGA

889

Db

481

TCAGACACCCCGCACATCCAGATTGGAGACATCCAGATGAGGCCACGAGGAGTGA

540

Qy

890

CCTAGTGAATGTGGGAGCTCTCTTCCCTCCACCCCTTCAATGCTTGCCTCTGCTC

949

Db

541

CCTAGTGAATGTGGGAGCTCTCTTCCCTCCACCCCTTCAATGCTTGCCTCTGCTC

600

Qy

950

TG 951

||

Db

601

TG 602

RESULT 10

AL559036

LOCUS

AL559036 Homo sapiens T CELLS (JURKAT CELL LINE) EST 31-MAY-2003

DEFINITION

Homo sapiens cDNA clone CS0DJ010YN13 5-PRIME, mRNA sequence.

ACCESSION

AL559036

VERSION

AL559036.2 GI:31283169

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

AUTHORS

Full-length cDNA libraries and normalization

TITLE

Unpublished (2001)

JOURNAL

On Feb 15, 2001 this sequence version replaced gi:12904138.

COMMENT

Contact: Genoscope

Genoscope, Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

8845.f For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DJ010CG07Qp1&cluster=8845.f. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Paraday Avenue Genoscope sequence ID : CS0DJ010CG07Qp1.

FEATURES

source

1..1022

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DJ010YN13"

/cell_type="T CELLS (JURKAT CELL LINE) EST 10-NORMALIZED"

/cell_line="JURKAT"

Qy

920

CCCCACCCCTTCATGGCTTGCCTCCTGCTCTCGGATTTTAGTGTGTGATTTCTGATCAG

979

Db

367

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426

Qy

980

GGATACCACTTCTGTGTCACACCCCGACCGGGCTAGAAAATTTGTTTGAGATTTTAT

1039

Db

427

GGATACCACTTCTGTGTCACACCCCGACCGGGCTAGAAAATTTGTTTGAGATTTTAT

486

Qy

1040

ATCATCTTGTCAAAATTTGCTTCAGTTGTAATGTGAAAAATGGGCTGGGGAAGGAGGTG

1099

Db

487

ATCATCTTGTCAAAATTTGCTTCAGTTGTAATGTGAAAAATGGGCTGGGGAAGGAGGTG

546

Qy

1100

TGTCCTAAATTTGTTTACTTCTTAACTTGTGTTTGTGCTTGGGCACTTGGCCTTTGTC

1159

Db

547

TGTCCTAAATTTGTTTACTTCTTAACTTGTGTTTGTGCTTGGGCACTTGGCCTTTGTC

606

Qy

1160

TGCTCTCAGTGTCTTCCCTTTGACATGGAAGAGTTGTGGCCAAAATCCCCATCTCT

1219

Db

607

TGCTCTCAGTGTCTTCCCTTTGACATGGAAGAGTTGTGGCCAAAATCCCCATCTCT

666

Qy

1220

TGCACCTCAAGCTGTGTGCTCAGGGCTGGGCTGCAGAGGAGGCGCTTCACTTATATC

1279

Db

667

TGCACCTCAAGCTGTGTGCTCAGGGCTGGGCTGCAGAGGAGGCGCTTCACTTATATC

726

Qy

1280

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1339

Db

727

TGTGTGTTATCCAGGGCTCCAGACTTCTCTCTGCTGCCCCACTGCACCTCTCCCC

786

Qy

1340

CTTATCTATCTCTTCTGCTTCCCGCCAGCCAGTCTTGGCTTCTTGTCCCTCCCTGGGT

1399

Db

787

CTTATCTATCTCTTCTGCTTCCCGCCAGCCAGTCTTGGCTTCTTGTCCCTCCCTGGGT

846

Qy

1400

CATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACAGGGCTGGCCAGTGGATT

1459

Db

847

CATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACAGGGCTGGCCAGTGGATT

906

Qy

1460

TCATGGTGATCATTTAAAAAGAAAAATCGCAACCAAAAAA 1505

Db

907

TCATGGTGATCATTTAAAAAGAAAAATCGCAACCAAAAAA 952

RESULT 11

BM717452

LOCUS

BM717452 Homo sapiens 649 bp mRNA linear EST 28-FEB-2002

DEFINITION

UI-E-EJ0-ahn-c-08-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone

UI-E-EJ0-ahn-c-08-0-UI 5', mRNA sequence.

ACCESSION

BM717452

VERSION

BM717452.1 GI:19030710

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE

1 (bases 1 to 649)

Bonaldi, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

JOURNAL

97044477

MEDLINE

8889548

PUBMED

Contact: Soares, MB

COMMENT

/clone lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

QY	1332	TCTGTGGCTCAGGGCTGGGTGGGAGAGGAGGCTTACCTTATATCTGTGTTGTTATC	1291
Db	361	TCTGTGGCTCAGGGCTGGGTGGGAGAGGAGGCTTACCTTATATCTGTGTTGTTATC	420
QY	1292	CAGGGCTCCAGACTTCTCTCTCTGCGCTGCGCCACTGCACCTCTCCCCCTTATCTATCTC	1351
Db	421	CAGGGCTCCAGACTTCTCTCTCTGCGCTGCGCCACTGCACCTCTCCCCCTTATCTATCTC	480
QY	1352	CTTCTCGGCTCCCGCAGCCAGCTTTGGCTTCTTGTCTCCCTCTCTGGGTCACTCCCTCCACT	1411
Db	481	CTTCTCGGCTCCCGCAGCCAGCTTTGGCTTCTTGTCTCCCTCTGGGTCACTCCCTCCACT	540
QY	1412	CTGACTCTGACTATGGCAGCAGAACACAGGCGCTGGCCAGTGGATTTTCATGGTGATCA	1471
Db	541	CTGACTCTGACTATGGCAGCAGAACACAGGCGCTGGCCAGTGGATTTTCATGGTGATCA	600
QY	1472	TTAAAAAGAAAAATCGCACCAAAAAA	1505
Db	601	TTAAAAAGAAAAATCGCACCAAAAAA	634
RESULT 12	BM674957/c		
LOCUS	BM674957	650 bp	mRNA
DEFINITION	UI-E-EJ0-ahn-c-08-0-UI.s1	UI-E-EJ0	Homo sapiens cDNA clone
ACCESSION	BM674957		
VERSION	BM674957.1	GI:18984855	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Bonaldo,M.F., Lennon,G. and Soares,M.B.		
	Normalization and subtraction: two approaches to facilitate gene		
	discovery		
JOURNAL	Genome Res. 6 (9), 791-806 (1996)		
MEDLINE	97044477		
PUBMED	8889548		
COMMENT	Contact: Soares, MB		
	Coordinated Laboratory for Computational Genomics		
	University of Iowa		
	375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA		
	Tel: 319 335 8250		
	Fax: 319 335 9565		
	Email: bento-soares@uiowa.edu		
	Tissue Procurement: Dr. Gregg Hageman		
	cDNA Library preparation: Dr. M. Bento Soares, University of Iowa		
	cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa		
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa		
	Clone Distribution: Researchers may obtain clones from Research		
	Genetics (www.resgen.com).		
	The following repetitive elements were found in this cDNA		
	sequence: 1-38, >POLY A#simple_repeat (matched complement)		
	Seq primer: M13 Forward		
	POLY A=Yes		
FEATURES	location/Qualifiers		
source	1..650		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="UI-E-EJ0-ahn-c-08-0-UI"		
	/tissue_type="fetal eyes, lens, eye anterior segment,		
	optic nerve, retina, Retina Foveal and Macular, RPE and		
	Choroid"		
	/dev_stage="fetal and adult"		
	/lab_host="DH10B (Life Technologies) (T1 phage resistant)"		
	/clone_lib="UI-E-EJ0"		
	/note="Organ: eye; Vector: pTT3-Pac (Pharmacia) with a		
	modified polylinker; Site 1: EcoR I; Site 2: Not I;		
	UI-E-EJ0 is a subtracted cDNA library constructed		

according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGAATAGCA; eye anterior segment, AATCCGCAT; optic nerve, CCATTAAGTG; retina, CGCGC; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG TISSUE=human retina TAG LIB=UI-E-E70 TAG_SEQ=CCGGC

ORIGIN		Query Match	38.6%; Score 581; DB 12; Length 650;
		Best Local Similarity	100.0%; Pred. No. 3.8e-187;
		Matches 581; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	925	CCCTTCATGGCTGCTCCTGCTCGATTTTAGGTGTGATTTCTGGATCAGCGGATA	984
Db	587	CCCTTCATGGCTGCTCCTGCTCGATTTTAGGTGTGATTTCTGGATCAGCGGATA	528
QY	985	CCACTTCCTGTCACACCCGACAGGGGCTAGAAAAATTTGTTGAGATTTTATATCAT	1044
Db	527	CCACTTCCTGTCACACCCGACAGGGGCTAGAAAAATTTGTTGAGATTTTATATCAT	468
QY	1045	CTTGTCAAATGCTTCAGTTGTAATGTGAAAAATGGCTGGGAAAGAGGTGTGTCC	1104
Db	467	CTTGTCAAATGCTTCAGTTGTAATGTGAAAAATGGCTGGGAAAGAGGTGTGTCC	408
QY	1105	CTAATGTTTACTGTGTAACCTGTTCTGTCCTCGGCACTTGGCTTTGCTGCTC	1164
Db	407	CTAATGTTTACTGTGTAACCTGTTCTGTCCTCGGCACTTGGCTTTGCTGCTC	348
QY	1165	TCAGTGTCTTCCCTTTGACATGGGAAAGAGGTGTGGCAAAATCCCATCTCTTTGAC	1224
Db	347	TCAGTGTCTTCCCTTTGACATGGGAAAGAGGTGTGGCAAAATCCCATCTCTTTGAC	288
QY	1225	CTCAACGCTGTGGCTCAGGGCTGGGTCGAGAGGAGGCTTACCTTATATCTGTCT	1284
Db	287	CTCAACGCTGTGGCTCAGGGCTGGGTCGAGAGGAGGCTTACCTTATATCTGTCT	228
QY	1285	TGTTATCCAGGGTCCAGACTTCTCTCTGCTGCTGCCCTGACCCCTCTCCCTTAT	1344
Db	227	TGTTATCCAGGGTCCAGACTTCTCTCTGCTGCTGCCCTGACCCCTCTCCCTTAT	168
QY	1345	CTATCTCTTCTCGGCTCCCGAGCCAGCTTTGGCTTTCTGTCCTCTCTGGGGTCATCC	1404
Db	167	CTATCTCTTCTCGGCTCCCGAGCCAGCTTTGGCTTTCTGTCCTCTCTGGGGTCATCC	108
QY	1405	CTCCACTCTGACTCTGACTATGTCACAGAACACAGGCGCTGGCCACAGTTTCATG	1464
Db	107	CTCCACTCTGACTCTGACTATGTCACAGAACACAGGCGCTGGCCACAGTTTCATG	48
QY	1465	GTGATCATTAATAAAGAAAAATCGCAACCAAAAAA	1505
Db	47	GTGATCATTAATAAAGAAAAATCGCAACCAAAAAA	7

RESULT 13
 BU624717/c
 LOCUS
 DEFINITION
 UI-H-FGI-bgi-h-13-0-UI.s1 NCI CGAP_FGI Homo sapiens cDNA clone
 UI-H-FGI-bgi-h-13-0-UI 3', mRNA sequence.
 BU624717
 VERSION
 BU624717.1 GI:23290932
 EST.
 KEYWORDS
 SOURCE
 Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 672)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: James Martin
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 Location/Qualifiers
 1..672
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clones="UI-H-FGI-bgi-h-13-0-UI"
 /tissue_type="Cell lines"
 /dev_stage="Adult"
 /lab_hosts="DH10B (Life Technologies)"
 /clone_lib="NCI-CGAP_FGI"
 /note="Organ: Enchondroma; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FGI is a normalized cDNA library obtained from a pool of mRNA from 2 cell lines from Enchondroma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGTCATC. The cell lines were provided by Dr. James Martin from the University of Iowa.
 TAG TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
 TAG LIB=UI-H-FGI
 TAG_SEQ=CGGTCATC

ORIGIN

		Query Match	38.3%; Score 576; DB 13; Length 672;
		Best Local Similarity	100.0%; Pred. No. 1.9e-185;
		Matches 576; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	915	TCCTCCCCACCCCTTCATGGCTTGGCTCTGCTCTGGATTTAGGTGTGATTTCTGA	974
Db	597	TCCTCCCCACCCCTTCATGGCTTGGCTCTGCTCTGGATTTAGGTGTGATTTCTGA	538
QY	975	TCACGGGATACCACTTCTGTCACACCCGACAGGGCTAGAAAAATTTGTTGAGATT	1034
Db	537	TCACGGGATACCACTTCTGTCACACCCGACAGGGCTAGAAAAATTTGTTGAGATT	478
QY	1035	TTTATATCATCTTGTCAAAATGCTTCAAGTTGTAATGTGAAAAATGGCTGGGAAAGA	1094
Db	477	TTTATATCATCTTGTCAAAATGCTTCAAGTTGTAATGTGAAAAATGGCTGGGAAAGA	418
QY	1095	GGTGGTGCTCCCTAATGTTTACTTGTAACTTGTCTGCTCCCTGGGCACTTGGCCT	1154
Db	417	GGTGGTGCTCCCTAATGTTTACTTGTAACTTGTCTGCTCCCTGGGCACTTGGCCT	358
QY	1155	TTGCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGTTGTGGCCAAAATCCCAT	1214
Db	357	TTGCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGTTGTGGCCAAAATCCCAT	298
QY	1215	CTTCTTGCACCTCAACGCTGTGTGGCTGAGGGCTGGCAGAGGAGGCGCTTCACCT	1274


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Db      297  CTTCTTGCACCTCAAGTCTGTGGCTCAGGGCTGGGGTGGCAGAGGAGGCGCTTCACTTT 238
QY      1275  ATATCTGTCTTGTATCCAGGGCTCCAGACTTCTCTCTCTGCTGCTGCCCACTGCACCTTC 1334
Db      237  ATATCTGTCTTGTATCCAGGGCTCCAGACTTCTCTCTCTGCTGCTGCCCACTGCACCTTC 178
QY      1335  TCCCTCTATCTATCTCTCTCTGCTGCTGCCCACTGCACCTTC 1394
Db      177  TCCCTCTATCTATCTCTCTCTGCTGCTGCCCACTGCACCTTC 118
QY      1395  GGGTCATCTCTCTCTCTGCTGCTGCCCACTGCACCTTC 1454
Db      117  GGGTCATCTCTCTCTCTGCTGCTGCCCACTGCACCTTC 58
QY      1455  GGATTTTCATCTCTCTCTCTGCTGCTGCCCACTGCACCTTC 1490
Db      57  GGATTTTCATCTCTCTCTCTGCTGCTGCCCACTGCACCTTC 22

RESULT 14
BUS39642
LOCUS      BUS39642
DEFINITION AGENCOURT_10224058 NIH_MGC_107 Homo sapiens cDNA clone
IMAGE:6570429 5', mRNA sequence.
ACCESSION BUS39642
VERSION    BUS39642.1 GI:22850083
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2759 row: e column: 21
High quality sequence stop: 527.
FEATURES   Location/Qualifiers
            source
            1..937
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:6570429"
            /tissue_type="adenocarcinoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_107"
            /note="Organ: breast; Vector: pOTB7; Site:1: EcoRI;
            Site:2: XhoI; cDNA made by oligo-dT priming.
            Directionally cloned into EcoRI/XhoI sites using the
            following 5' adaptor: GGCAGGAG(G). Library constructed by
            Ling Hong in the laboratory of Gerald M. Rubin (University
            of California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies).
            Note: this is a NIH_MGC Library."

ORIGIN
Query Match      38.2%; Score 575; DB 13; Length 937;
Best Local Similarity 100.0%; Pred. No. 3.5e-185;
Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      135  GTGCGCGACCGCTGCGCTGTGTGAGCGGGGCTCGGGGGGATCGCGCGCGCTGGC 194
Db      1  GTGCGCGACCGCTGCGCTGTGTGAGCGGGGCTCGGGGGGATCGCGCGCGCTGGC 60

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QY      195  CCGGGCCCTGTGTCAGAGGACTGAAGGTGTGGCTCGGCCGCACTGTGGGCAACAT 254
Db      61  CCGGGCCCTGTGTCAGAGGACTGAAGGTGTGGCTCGGCCGCACTGTGGGCAACAT 120
QY      255  CCAGAGAGCTGGCTGTGAATGTAAGAGTGCAGGCTACCCCGGAGCTTTGATCCCTACAG 314
Db      121  CCAGAGAGCTGGCTGTGAATGTAAGAGTGCAGGCTACCCCGGAGCTTTGATCCCTACAG 180
QY      315  ATGTGACCTATCAATGAAGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCA 374
Db      181  ATGTGACCTATCAATGAAGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCA 240
QY      375  CAGCGGTGTAGACATCTGTGATCAACAATGCTGGCTTGGCCGCTGCACACCTGTCTC 434
Db      241  CAGCGGTGTAGACATCTGTGATCAACAATGCTGGCTTGGCCGCTGCACACCTGTCTC 300
QY      435  AGGCAGACACCATGTTGGAAGGACATCTTCAATGTGAACGTGCTGGCCCTCAGCATCTG 494
Db      301  AGGCAGACACCATGTTGGAAGGACATCTTCAATGTGAACGTGCTGGCCCTCAGCATCTG 360
QY      495  CACCGGAAGCCTACCATGAAGAGGCGGAATGTGGACGATGGGCACATCATTA 554
Db      361  CACCGGAAGCCTACCATGAAGAGGCGGAATGTGGACGATGGGCACATCATTA 420
QY      555  CATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACCCACTTCTATAGTGC 614
Db      421  CATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACCCACTTCTATAGTGC 480
QY      615  CACCAAGTATCCGCTCACTGCGTGACAGAGGAGTGAAGAGCTTCGGGAGGCCCA 674
Db      481  CACCAAGTATCCGCTCACTGCGTGACAGAGGAGTGAAGAGCTTCGGGAGGCCCA 540
QY      675  GACCCACATCCGAGCCACGTCATCTCTCCAGGTG 709
Db      541  GACCCACATCCGAGCCACGTCATCTCTCCAGGTG 575

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RESULT 15
BM742038
LOCUS      BM742038
DEFINITION K-EST0014773 S1SNU5s1 Homo sapiens cDNA clone S1SNU5s1-1-B09 5',
            mRNA sequence.
ACCESSION BM742038
VERSION    BM742038.1 GI:19063367
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 573)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 1 row: B column: 09
High quality sequence stop: 573.
FEATURES   Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="S1SNU5s1-1-B09"
            /sex="F"
            /tissue_type="Ascites"

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remaining DNA into competent cells E. coli Top10F' with electroporation method."

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ORIGIN
Query Match      37.6%; Score 566; DB 12; Length 566;
Best Local Similarity 100.0%; Pred. No. 5e-182;
Matches 566; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 TGTCTCAGCATATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGCT 409
Db 1 TGTCTCAGCATATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGCT 60
QY 410 TGGCCGGGCTGACACCCCTGCTCTCAGGAGCAGCAGTGTGGAAGGACATGTTCAATG 469
Db 61 TGGCCGGGCTGACACCCCTGCTCTCAGGAGCAGCAGTGTGGAAGGACATGTTCAATG 120
QY 470 TGAAGCTGTGGCCCTCAGCATCTGACACCGGGAAGCCATCCAGTCCATGAAGGAGCGGA 529
Db 121 TGAACGTGTGGCCCTCAGCATCTGACACCGGGAAGCCATCCAGTCCATGAAGGAGCGGA 180
QY 530 ATGTGGACGATGGGCACATCAATACATCAATAGCATGTCGGCCACCGAGTGTACCCC 589
Db 181 ATGTGGACGATGGGCACATCAATACATCAATAGCATGTCGGCCACCGAGTGTACCCC 240
QY 590 TGTCTGTGACCATCTTATAGTGCCACCAAGTATGCCGTCACTCGCTGACAGAGGAC 649
Db 241 TGTCTGTGACCATCTTATAGTGCCACCAAGTATGCCGTCACTCGCTGACAGAGGAC 300
QY 650 TGAGCAAGAGCTTCGGAGGCCAGACCCACATCCGAGCCACAGTGCATCTCCAGGTG 709
Db 301 TGAGCAAGAGCTTCGGAGGCCAGACCCACATCCGAGCCACAGTGCATCTCCAGGTG 360
QY 710 TGGTGGAGACAAATTCGCTTCAAACCTCCAGCAAGGAGGAGTGTGGCGAGGCTGTATCTACGTCC 829
Db 361 TGGTGGAGACAAATTCGCTTCAAACCTCCAGCAAGGAGGAGTGTGGCGAGGCTGTATCTACGTCC 420
QY 770 CCTATGACAAATGAAGTGTCTCAAACCGAGGAGTGTGGCGAGGCTGTATCTACGTCC 829
Db 421 CCTATGACAAATGAAGTGTCTCAAACCGAGGAGTGTGGCGAGGCTGTATCTACGTCC 480
QY 830 TCAGACCCCGCAGACATCCAGATTTGAGACATCCAGATGAGGCCCGCAGGAGGTGA 889
Db 481 TCAGACCCCGCAGACATCCAGATTTGAGACATCCAGATGAGGCCCGCAGGAGGTGA 540
QY 890 CCTATGACTGTGGAGTCTCCTCTT 915
Db 541 CCTATGACTGTGGAGTCTCCTCTT 566

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RESULT 17
LOCUS BG030249 912 bp mRNA linear EST 24-JAN-2001
DEFINITION 602297547F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4392011 5',
mRNA sequence.
ACCESSION BG030249
VERSION BG030249.1 GI:12419347
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 932)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

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http://image.llnl.gov
Plate: LLAMI0083 row: n column: 12
High quality sequence stop: 601.

FEATURES

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1..932
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4392011"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

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ORIGIN

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Query Match      36.1%; Score 543; DB 10; Length 932;
Best Local Similarity 100.0%; Pred. No. 2.6e-174;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 TGCTGAATGTAAGAGTGAGGCTACCCCGGAGCTTGTGATCCCTACAGATGTGACCTATC 326
Db 13 TGCTGAATGTAAGAGTGAGGCTACCCCGGAGCTTGTGATCCCTACAGATGTGACCTATC 72
QY 327 AAATGAAGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCAGCGGTGTAGA 386
Db 73 AAATGAAGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCAGCGGTGTAGA 132
QY 387 CATCTGATCAACAATGCTGGCTTGGCCCGGCTGACACCTGCTCTCAGGAGCACCAG 446
Db 133 CATCTGATCAACAATGCTGGCTTGGCCCGGCTGACACCTGCTCTCAGGAGCACCAG 192
QY 447 TGGTTGGAAGGACATGTTCAATGTGAAGTGTGGCCCGGCTGACACCTGCTCTCAGGAGCACCAG 506
Db 193 TGGTTGGAAGGACATGTTCAATGTGAAGTGTGGCCCGGCTGACACCTGCTCTCAGGAGCACCAG 252
QY 507 CTACCACTCCATGAAGGAGCGAATGTGGAGCATGGGCACATCAATCAATCAATAGCAT 566
Db 253 CTACCACTCCATGAAGGAGCGAATGTGGAGCATGGGCACATCAATCAATCAATAGCAT 312
QY 567 GTCTGGCCACCGAGTGTACCCCTGTCTGTGACCCACTTCTATAGTCCACCAAGTATGC 626
Db 313 GTCTGGCCACCGAGTGTACCCCTGTCTGTGACCCACTTCTATAGTCCACCAAGTATGC 372
QY 627 CGTCACCTGCGCTGACAGAGGAGCTGAGGAGAGCTTGGGAGGCCCGCAGCCACATCCG 686
Db 373 CGTCACCTGCGCTGACAGAGGAGCTGAGGAGAGCTTGGGAGGCCCGCAGCCACATCCG 432
QY 687 AGCCACCTGATCTCTCCAGGTGTGGTGGAGACACAATTCGCCCTTCAAACCTCCACGCAA 746
Db 433 AGCCACCTGATCTCTCCAGGTGTGGTGGAGACACAATTCGCCCTTCAAACCTCCACGCAA 492
QY 747 GGACCCCTGAGAGGAGCTGCGACCTATGAGCAAAATGAAGTGTCTCAAAACCCGAGGATGT 806
Db 493 GGACCCCTGAGAGGAGCTGCGACCTATGAGCAAAATGAAGTGTCTCAAAACCCGAGGATGT 552
QY 807 GGC 809
Db 553 GGC 555

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RESULT 18
LOCUS BG231973/c 541 bp mRNA linear EST 09-FEB-2001
DEFINITION naf34g12.x1 Soares_NPBMC Homo sapiens cDNA clone IMAGE:4143166 3',
mRNA sequence.
ACCESSION BG231973
VERSION BG231973.1 GI:12727118
KEYWORDS EST.
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 541)
REFERENCE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D. and M. Patima
Bonaldo, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Seq primer: -400P from Gibco
High quality sequence stop: 480.
Location/Qualifiers
1. 541
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4143166"
/tissue_type="lymphocyte"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Soares NPBMC"
/note="Organ: blood; Vector: pT7D-Pac; Site 1: Not I;
Site 2: EcoRI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCCGCCGCGGTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
is normalized; constructed in the laboratory of M. Bento
Soares (University of Iowa)."

FEATURES
source
1. 541
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4143166"
/tissue_type="lymphocyte"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Soares NPBMC"
/note="Organ: blood; Vector: pT7D-Pac; Site 1: Not I;
Site 2: EcoRI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCCGCCGCGGTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
is normalized; constructed in the laboratory of M. Bento
Soares (University of Iowa)."

ORIGIN
Query Match 35.9%; Score 541; DB 12; Length 541;
Best Local Similarity 100.0%; Pred. No. 1.6e-173; Indels 0; Gaps 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 952 GATTTTAGTGTGTTGATTTCTGGATCACGGGATACCACTTCCTGTCACACCCCGACGAG 1011
DB 541 GATTTTAGTGTGTTGATTTCTGGATCACGGGATACCACTTCCTGTCACACCCCGACGAG 482
QY 1012 GCTAGAAAATTTGTTTGAGATTTTATATCATCTGTCAAAATTCCTCAGTTGTAATG 1071
DB 481 GCTAGAAAATTTGTTTGAGATTTTATATCATCTGTCAAAATTCCTCAGTTGTAATG 422
QY 1072 TGAATAATGGCTGGGGAAGAGGTGGTGTCCCTAAATGTTTACTTGTAACTTGTTC 1131
DB 421 TGAATAATGGCTGGGGAAGAGGTGGTGTCCCTAAATGTTTACTTGTAACTTGTTC 362
QY 1132 TTGTGCCCCCTGGGCACTTGGCCCTTGTCTGCTCTAGTGTCTCCCTTTGACATGGGAAA 1191
DB 361 TTGTGCCCCCTGGGCACTTGGCCCTTGTCTGCTCTAGTGTCTCCCTTTGACATGGGAAA 302
QY 1192 GGAGTTGTGGCCAAATCCCAATCTCTTTCGACCTCAAGCTGTGGCTCAGGCTGGGG 1251
DB 301 GGAGTTGTGGCCAAATCCCAATCTCTTTCGACCTCAAGCTGTGGCTCAGGCTGGGG 242
QY 1252 TGGCAGAGGAGGCGCTTACCTTATATCTGTGTGTATCCAGGGCTCCAGACTTCCTCC 1311
DB 241 TGGCAGAGGAGGCGCTTACCTTATATCTGTGTGTATCCAGGGCTCCAGACTTCCTCC 182
QY 1312 TCTGCTGCCCGCACTGCAGCCCTCTCCCTTATCTATCTCTTCTGGCTCCCGACCCA 1371
DB 181 TCTGCTGCCCGCACTGCAGCCCTCTCCCTTATCTATCTCTTCTGGCTCCCGACCCA 122
QY 1372 GTCTTGGCTTCTTGTCCCTCTGGGGTGCATCCCTCCACTCTGACTCTGACTATGGCAGC 1431

Db 121 GTCTTGCTCTTGTCCCTCTGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGC 62
QY 1432 AGAACACAGGCGCTGGCCAGTGGATTTCATGTGTATCATTAATAAGAAAAATCGAA 1491
DB 61 AGAACACAGGCGCTGGCCAGTGGATTTCATGTGTATCATTAATAAGAAAAATCGAA 2
QY 1492 C 1492
DB 1 C 1
RESULT 19
BM737591
LOCUS K-EST0000094 S1SNUS Homo sapiens cDNA clone S1SNUS-21-B02 5', mRNA
DEFINITION sequence.
ACCESSION BM737591
VERSION BM737591.1 GI:19058920
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
REFERENCE Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 21 row: B column: 02
High quality sequence stop: 582.
Location/Qualifiers
1. 582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S1SNUS-21-B02"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/cell_line="SNU-5"
/lab_host="Top10F"
/clone_lib="S1SNUS"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then dephosphorylated
with tabacco acid pyrophosphatase (TAP). The dephosphorylated
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN
Query Match 35.3%; Score 531; DB 12; Length 582;
Best Local Similarity 99.8%; Pred. No. 3.8e-170; Indels 0; Gaps 0;
Matches 581; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongjung@mail.kribb.re.kr
Plate: 58 row: C column: 04
High quality sequence stop: 540.

FEATURES

Location/Qualifiers
1. 540
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-58-C04"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10P"
/clone_lib="S13KMS5"
/note="Vector: PCNS; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 34.3%; Score 516; DB 12; Length 540;
Best Local Similarity 100.0%; Pred. No. 4.9e-165;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AAGCAGGTCTGGCGCGCGCAGGAGCGCGCGCTCAGTCTCTCGACCCCGTGTCT 74
DB 1 AAGCAGGTCTGGCGCGCGCGCAGGAGCGCGCGCTCAGTCTCTCGACCCCGTGTCT 60

QY 75 GGGCTAGTCTCAGCAGGCGGACCGGGGGTGGGCGCCATGGCCAGCGCGCGGATGGAGCG 134
DB 61 GGGCTAGTCTCAGCAGGCGGACCGGGGGTGGGCGCCATGGCCAGCGCGCGGATGGAGCG 120

QY 135 GTGGCGGACCGGCTGGGCGCTGTGACGGGGGCGCTCGGGGGCATCGGCGCGCGTGGC 194
DB 121 GTGGCGGACCGGCTGGGCGCTGTGACGGGGGCGCTCGGGGGCATCGGCGCGCGTGGC 180

QY 195 CGGGGCCCTGTGTCAGCAGGAGCTGAAGTGTGTGGGTGCGCCCGCATGTGGGCAACAT 254
DB 181 CGGGGCCCTGTGTCAGCAGGAGCTGAAGTGTGTGGGTGCGCCCGCATGTGGGCAACAT 240

QY 255 CGAGAGCTGGTGTCTGAATCTAAGTGTGAGCTACCCCGGACTTTGATCCCTACAG 314
DB 241 CGAGAGCTGGTGTCTGAATCTAAGTGTGAGCTACCCCGGACTTTGATCCCTACAG 300

QY 315 ATGTGACCTTCAATGAAGAGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCA 374
DB 301 ATGTGACCTTCAATGAAGAGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCA 360

QY 375 CAGCGGTGTAGACATCTGCATCAACATCTGGTGGCCCGGCTGACACCCCTGCTCTC 434
DB 361 CAGCGGTGTAGACATCTGCATCAACATCTGGTGGCCCGGCTGACACCCCTGCTCTC 420

QY 435 AGGCAGCACAGTGGTTGAAGACATGTTCAATGTGAACGTGTGGCCCTCAGCATCTG 494
DB 421 AGGCAGCACAGTGGTTGAAGACATGTTCAATGTGAACGTGTGGCCCTCAGCATCTG 480

QY 495 CACACGGGAGCCTACCACTCCATGAAGAGCGGAA 530
|||||

Db 481 CACACGGGAGCCTACCACTCCATGAAGAGCGGAA 516

RESULT 22
BM682228/c
LOCUS
DEFINITION
UI-E-EJ0-aio-j-09-0-UI.s1 UI-E-EJ0 Homo sapiens cDNA clone
UI-E-EJ0-aio-j-09-0-UI 3', mRNA sequence.
ACCSSION
BM682228
VERSION
BM682228.1 GI:18992124
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 572)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
97044477
MEDLINE
PUBMED
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road. 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-38, >POLY A#Simple_repeat (matched complement)
Seq primer: M13 Forward
POLYA=Yes.

FEATURES

Location/Qualifiers
1. 572
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ0-aio-j-09-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stages="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ0"
/note="Organ: eye; Vector: pT7T3-Pac (pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EJ0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGAATCAGA; lens, CGATTAGCGA; eye anterior segment,
AATGCCGAT; optic nerve, CCATTAGTG; retina, CCGCG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI).
TAG TISSUE=human retina
TAG_LIB=UI-E-EJ0
TAG_SEQ=CCGCG"

ORIGIN

```
Query Match      34.2%; Score 515; DB 12; Length 572;
Best Local Similarity 99.8%; Pred. No. 1e-164;
Matches 565; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 940 CTCCTGCTCTGGATTTAGGTGTTGATTTCTGGATACGGGATACCACTTCTCTCCAC 999
Db 572 CTCCTGCTCTGGATTTAGGTGTTGATTTCTGGATACGGGATACCACTTCTCTCCAC 513

QY 1000 ACCCGACACAGGGCTAGAAAATTTGTTGAGATTTTATATATCATCTTGTCAATGCTT 1059
Db 512 ACCCGACACAGGGCTAGAAAATTTGTTGAGATTTTATATATCATCTTGTCAATGCTT 453

QY 1060 CAGTTGTAATGTGAAAATGGGCTGGGAAAGAGGTGGTGTCCCTAATGTTTACTT 1119
Db 452 CAGTTGTAATGTGAAAATGGGCTGGGAAAGAGGTGGTGTCCCTAATGTTTACTT 393

QY 1120 GTTAACCTGTTCTTGCCCTGGGACCTGGCTTTGCTGCTCTCAGTGTCTTCCCTT 1179
Db 392 GTTAACCTGTTCTTGCCCTGGGACCTGGCTTTGCTGCTCTCAGTGTCTTCCCTT 333

QY 1180 TGACATGGGAAAGAGTTGTGGCCAAATCCCATCTTCTTGCACCTCAAGTCTGTGGC 1239
Db 332 TGACATGGGAAAGAGTTGTGGCCAAATCCCATCTTCTTGCACCTCAAGTCTGTGGC 273

QY 1240 TCAGGCTGGGTGGCAGAGGAGGCTTTCACCTTATATCTGTGTGTTATCCAGGGCTC 1299
Db 272 TCAGGCTGGGTGGCAGAGGAGGCTTTCACCTTATATCTGTGTGTTATCCAGGGCTC 213

QY 1300 CAGACTTCTCTCTGCTGCTGCCACCTGACACCTCTCCCTTATCTATCTCTCTCTCGG 1359
Db 212 CAGACTTCTCTCTGCTGCTGCCACCTGACACCTCTCCCTTATCTATCTCTCTCTCGG 153

QY 1360 CTCCTCCAGCCAGCTTGGCTTCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1419
Db 152 CTCCTCCAGCCAGCTTGGCTTCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 93

QY 1420 GACTATGGCAGCAGAACACAGGCGCTGGCCAGTGGATTTTCATGGTGATCATTAATAA 1479
Db 92 GACTATGGCAGCAGAACACAGGCGCTGGCCAGTGGATTTTCATGGTGATCATTAATAA 33

QY 1480 GAAAAATCGCAACCAAAAAA 1505
Db 32 GAAAAATCGCAACCAAAAAA 7

RESULT 23
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LOCUS
DEFINITION K-EST0016711 S1SNUS1 Homo sapiens mRNA linear EST 01-MAR-2002
mRNA sequence.
BM743569
VERSION BM743569.1 GI:19064898
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 550)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.krrib.re.kr
Plate: 5 row: C column: 01
High quality sequence stop: 550.
Location/Qualifiers
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source

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1..550
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S1SNUS1-5-C01"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/lab_host="SNU-5"
/clone_lib="S1SNUS1"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and
sequencing about 2,000 ~ 3,000 colonies in original cDNA
library, the abundant cDNAs were selected and amplified by
PCR reaction using vector region primer including T7
promotor as 5' primer and N(dn)14 as 3' primer. The PCR
products were used as template for synthesis of
biotinylated single stranded RNA by in vitro transcription
reaction. The synthesized RNA probes were hybridized with
antisense single stranded cDNAs prepared from original
library and incubated with avidin-gel. After removing
DNA-RNA hybrids by centrifuge, the subtracted cDNA
libraries were constructed by transformation of the
remaining DNA into competent cells E. coli Top10F' with
electroporation method."
```

ORIGIN

```
Query Match      34.0%; Score 511; DB 12; Length 550;
Best Local Similarity 100.0%; Pred. No. 2.4e-163;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 CTGCATCAACAATGCTGGCTTGGCCGGCTGACACCTCTCTCAGGACGACCACTGG 449
Db 40 CTGCATCAACAATGCTGGCTTGGCCGGCTGACACCTCTCTCAGGACGACCACTGG 99

QY 450 TTGGAAGGACATGTTCAATGTGAACGTTGCTGGCCCTCAGCATCTGCACGGGAAGCCTA 509
Db 100 TTGGAAGGACATGTTCAATGTGAACGTTGCTGGCCCTCAGCATCTGCACGGGAAGCCTA 159

QY 510 CCAGTCCATGAAGAGCGGAATGTGACGATGGGCATCATTAACATCAATAGCATGTC 569
Db 160 CCAGTCCATGAAGAGCGGAATGTGACGATGGGCATCATTAACATCAATAGCATGTC 219

QY 570 TGGCCACCGAGTGTATCCCTCTGTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGT 629
Db 220 TGGCCACCGAGTGTATCCCTCTGTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGT 279

QY 630 CACTGCGCTGACAGGGGACTGAGGCAAGAGCTTCGGGAGGCGCCAGACCCACATCCGAGC 689
Db 280 CACTGCGCTGACAGGGGACTGAGGCAAGAGCTTCGGGAGGCGCCAGACCCACATCCGAGC 339

QY 690 CAGTGCATCTCTCCAGGTGTGGTGAGACAAATTCGCTTCAAACTCCACGACAAGGA 749
Db 340 CAGTGCATCTCTCCAGGTGTGGTGAGACAAATTCGCTTCAAACTCCACGACAAGGA 399

QY 750 CCTGGAAGAGGAGCTGCCACCTATGAGCAAAATGAAGTGTCTCAAAACCCGAGGATGGC 809
Db 400 CCTGGAAGAGGAGCTGCCACCTATGAGCAAAATGAAGTGTCTCAAAACCCGAGGATGGC 459
```

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810 CGAGGCTGTTATCTACCTCTAGCACCCCGCACACATCCAGATTGGAGATCCAGAT 869
      |||
460 CGAGGCTGTTATCTACCTCTAGCACCCCGCACACATCCAGATTGGAGATCCAGAT 519
      |||
870 GAGGCCACGAGGAGGAGTGAAGTACTGACTG 900
      |||
520 GAGGCCACGAGGAGGAGTGAAGTACTGACTG 550

RESULT 24
BE386240
LOCUS
DEFINITION BE386240 769 bp mRNA linear EST 21-JUL-2000
601273447F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614770 5',
mRNA sequence.
ACCESSION BE386240
VERSION BE386240.1 GI:9331605
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 769)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM277 row: m column: 11
High quality sequence stop: 652.
FEATURES
Location/Qualifiers
1..769
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3614770"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

```

Query Match 33.0%; Score 496; DB 10; Length 769;
Best Local Similarity 100.0%; Pred. No. 2.6e-158;
Matches 496; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 800 AGGATGTGGCCGAGGCTGTTATCTAGCTCCTCAGCACCCCGCACACATCCAGATTGGAG 859
      |||
Db 1 AGGATGTGGCCGAGGCTGTTATCTAGCTCCTCAGCACCCCGCACACATCCAGATTGGAG 60
      |||
QY 360 ACATCCAGATGAGGCCCGCAGGAGGAGTGAAGTACTGAGTGTGGAGTCTCTCTCCCT 919
      |||
Db 61 ACATCCAGATGAGGCCCGCAGGAGGAGTGAAGTACTGAGTGTGGAGTCTCTCTCCCT 120
      |||
QY 920 CCCACCCCTTCTAGCTTCCCTCCCTCCCTGAGTTGAGTTGAGTTCTGGATCAGC 979
      |||
Db 121 CCCACCCCTTCTAGCTTCCCTCCCTCCCTGAGTTGAGTTGAGTTCTGGATCAGC 180
      |||
QY 980 GGATACCACTTCTGTTCCACACCCCGCAGGAGGCTAGAAAAATTTGTTGAGATTTTAT 1039
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```

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Db 181 GGATACCACTTCTGTTCCACACCCCGCAGGAGGCTAGAAAAATTTGTTGAGATTTTAT 240
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QY 1040 ATCATCTTGTCAAAATGCTTCACTTGTAAATGTCAAAAATGGGTGGGAAAGGAGGTGG 1059
      |||
Db 241 ATCATCTTGTCAAAATGCTTCACTTGTAAATGTCAAAAATGGGTGGGAAAGGAGGTGG 300
      |||
QY 1100 TGTCCCTCAATTTGTTTACTTGTAACTTGTCTTGTGCCCTTGGGCACACTTGGCCTTTGTC 1159
      |||
Db 301 TGTCCCTCAATTTGTTTACTTGTAACTTGTCTTGTGCCCTTGGGCACACTTGGCCTTTGTC 360
      |||
QY 1160 TGTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGTTGTGGCAAAATCCCAATCTTCT 1219
      |||
Db 361 TGTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGTTGTGGCAAAATCCCAATCTTCT 420
      |||
QY 1220 TGCACCTCAACGCTGTGGCTCAGGCTGGGTGGCGAGAGGAGGCTTCCACCTTATATC 1279
      |||
Db 421 TGCACCTCAACGCTGTGGCTCAGGCTGGGTGGCGAGAGGAGGCTTCCACCTTATATC 480
      |||
QY 1280 TGTGTTCTTATCCAGG 1295
      |||
Db 481 TGTGTTCTTATCCAGG 496
      |||

RESULT 25
A1125225/c
LOCUS
DEFINITION A1125225 489 bp mRNA linear EST 28-OCT-1998
qdb7f01.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1736473
3', mRNA sequence.
ACCESSION A1125225
VERSION A1125225.1 GI:3593739
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 489)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 598 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 465.
FEATURES
Location/Qualifiers
1..489
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1736473"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis_NHT"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5].
TGTACCAATCGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3'}.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."
```

ORIGIN


```

Query Match      32.5%; Score 489; DB 9; Length 489;
Best Local Similarity 100.0%; Pred. No. 7.6e-156;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1013 GCTAGAAAATTTGTTGAGATTTTATATCATCTTGTCAAAATGCTTCAGTTGTAAATGT 1072
Db 489 GCTAGAAAATTTGTTGAGATTTTATATCATCTTGTCAAAATGCTTCAGTTGTAAATGT 430

QY 1073 GAAATATGGCTGGGGAAGAGGAGGCTGCTCCCTAATTTGTTTACTGTTAACTTGTCT 1132
Db 429 GAAATATGGCTGGGGAAGAGGAGGCTGCTCCCTAATTTGTTTACTGTTAACTTGTCT 370

QY 1133 TGTGCCCCCTGGGCACTTGGCCCTTCTGCTCTCAAGTGTCTTCCCTTTGACATGGGAAG 1192
Db 369 TGTGCCCCCTGGGCACTTGGCCCTTGTCTGCTCTCAAGTGTCTTCCCTTTGACATGGGAAG 310

QY 1193 GAGTTGTGGCCAAATATCCCACTTCTTTCGACCTCAACGTCGTGGCTCAGGGCTGGGGT 1252
Db 309 GAGTTGTGGCCAAATATCCCACTTCTTTCGACCTCAACGTCGTGGCTCAGGGCTGGGGT 250

QY 1253 GGCAGAGGAGGCTTCACCTTATCTGTGTTTATCCAGGCTCCAGACTTCTCTCT 1312
Db 249 GGCAGAGGAGGCTTCACCTTATCTGTGTTTATCCAGGCTCCAGACTTCTCTCT 190

QY 1313 CTGCTGCCCCCACTGCACCCCTCTCCCCCTTATCTATCTCTCTGCTTCCGCTCCCGCCAG 1372
Db 189 CTGCTGCCCCCACTGCACCCCTCTCCCCCTTATCTATCTCTCTGCTTCCGCTCCCGCCAG 130

QY 1373 TCTTGGCTTCTGTCCTCTCTGGGTCATCCCTCCACTCTGACTCTGACTATGCGACGA 1432
Db 129 TCTTGGCTTCTGTCCTCTCTGGGTCATCCCTCCACTCTGACTCTGACTATGCGACGA 70

QY 1433 GAACACAGGCGCTGGCCAGTGAATTCATGGTGATCATTTAAAAAGAAAAATCGCAAC 1492
Db 69 GAACACAGGCGCTGGCCAGTGAATTCATGGTGATCATTTAAAAAGAAAAATCGCAAC 10

QY 1493 CAAAAAAA 1501
Db 9 CAAAAAAA 1

RESULT 26
CA424831/c
LOCUS
DEFINITION
  UI-H-FEI-bdw-e-17-0-UI.s1 NCI CGAP_FEI Homo sapiens cDNA clone
  UI-H-FEI-bdw-e-17-0-UI 3', mRNA sequence.
ACCESSION
  CA424831
VERSION
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1. (bases 1 to 566)
  NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-rc@mail.nih.gov
  Tissue Procurement: James Martin
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Clone distribution information can be obtained
  from Dr. M. Bento Soares, bento-soares@uiowa.edu
  Seq primer: M13 FORWARD
  POLYA=Yes.
FEATURES
  Location/Qualifiers
  source
    1..566
    /organism="Homo sapiens"
    /mol_type="mRNA"

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/db_xref="taxon:9606"
/clone="UI-H-FEI-bdw-e-17-0-UI"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_FEI"
/note="Organ: Chondrosarcoma; Vector: pTT3-Pac
(Pharmacia) with a modified polylinker; Site 1: Ecor I;
Site 2: Not I; NCI CGAP_FEI is a normalized cDNA library
derived from a pool of mRNA obtained from 3 cell lines
from grade II chondrosarcoma tissues. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an Ecor I
adaptor, digested with Not I, and cloned directionally
into pTT3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
CGTACCGAC. The cell lines were provided by Dr James
Martin from the University of Iowa.
TAG_TISSUE=Human grade 2 chondrosarcoma cell line pool
TAG_LIB=UI-H-FEI
TAG_SEQ=CGCTACGGAC"

ORIGIN
Query Match      32.5%; Score 489; DB 14; Length 566;
Best Local Similarity 100.0%; Pred. No. 7.1e-156;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 952 GATTTTAGGTGTTGATTTCTGGATCAGGGATACCACTTCCTGTCACACCCGACACGAG 1011
Db 566 GATTTTAGGTGTTGATTTCTGGATCAGGGATACCACTTCCTGTCACACCCGACACGAG 507

QY 1012 GGCTAGAAAATTTGTTGAGATTTTATATCATCTTGTCAAAATGCTTCAGTTGTAAATG 1071
Db 506 GGCTAGAAAATTTGTTGAGATTTTATATCATCTTGTCAAAATGCTTCAGTTGTAAATG 447

QY 1072 TGAATAATGGCTGGGGAAGAGGAGTGGTGTCCCTAATTTGTTTACTTGTAACTTGTTC 1131
Db 446 TGAATAATGGCTGGGGAAGAGGAGTGGTGTCCCTAATTTGTTTACTTGTAACTTGTTC 387

QY 1132 TTGTGCCCCCTGGGCACTTGGCCCTTGTCTCTCTCAAGTGTCTTCCCTTTGACATGGGAAA 1191
Db 386 TTGTGCCCCCTGGGCACTTGGCCCTTGTCTCTCTCAAGTGTCTTCCCTTTGACATGGGAAA 327

QY 1192 GGAGTTGTGGCCAAATATCCCACTTCTTGCACCTCAACGTCGTGGCTCAGGGCTGGGG 1251
Db 326 GGAGTTGTGGCCAAATATCCCACTTCTTGCACCTCAACGTCGTGGCTCAGGGCTGGGG 267

QY 1252 TGGCAGAGGAGGCGCTTCACCTTATATCTGTGTTGTTTATCCAGGCTCCAGACTTCTCTC 1311
Db 266 TGGCAGAGGAGGCGCTTCACCTTATATCTGTGTTGTTTATCCAGGCTCCAGACTTCTCTC 207

QY 1312 TCTGCTGCCCCCACTGCACCCCTCTCCCTCTTATCTATCTCTCTCGGTCCCGACGCCA 1371
Db 206 TCTGCTGCCCCCACTGCACCCCTCTCCCTCTTATCTATCTCTCTCGGTCCCGACGCCA 147

QY 1372 GTCTTGGCTTCTTGTCCCTCTGCTGGGTCATCCCTCACTCTGACTCTGACTATGCGAGC 1431
Db 146 GTCTTGGCTTCTTGTCCCTCTGCTGGGTCATCCCTCACTCTGACTCTGACTATGCGAGC 87

QY 1432 AGAACACCA 1440
Db 86 AGAACACCA 78

RESULT 27
BM723373
LOCUS
DEFINITION
  UI-E-EJO-aio-j-09-0-UI.r1 UI-E-EJO Homo sapiens cDNA clone
  UI-E-EJO-aio-j-09-0-UI 5', mRNA sequence.

```

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RESULT 27
BM723373
LOCUS
DEFINITION
  UI-E-EJO-aio-j-09-0-UI.r1 UI-E-EJO Homo sapiens cDNA clone
  UI-E-EJO-aio-j-09-0-UI 5', mRNA sequence.

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ORIGIN

Query Match	31.7%;	Score 477;	DB 10;	Length 513;
Best Local Similarity	100.0%;	Pred. No. 8.e-152;		
Matches 477;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	782	TGAAGTGCTCAAAACCCAGAGATGTGGCCGAGGCTGTTATCTAGTCCTCAGCACCCCCG	841	
Db	1	TGAAGTGCTCAAAACCCAGAGATGTGGCCGAGGCTGTTATCTAGTCCTCAGCACCCCCG	60	
QY	842	CACACATCCAGATTGGAGACATCCAGATGAGCCACGAGCAGGTGACCTAGTGACTGT	901	
Db	61	CACACATCCAGATTGGAGACATCCAGATGAGCCACGAGCAGGTGACCTAGTGACTGT	120	
QY	902	GGGAGCTCCTCTTCCCTCCCAACCCCTTCATGGCTTGCCCTCCTGCCCTCTGGATTTTAGGT	961	
Db	121	GGGAGCTCCTCTTCCCTCCCAACCCCTTCATGGCTTGCCCTCCTGCCCTCTGGATTTTAGGT	180	
QY	962	GTTGATTTCTGGATCAGGGATACCACTTCTGTGCCACACCCACAGGGGCTAGAAAA	1021	
Db	181	GTTGATTTCTGGATCAGGGATACCACTTCTGTGCCACACCCACAGGGGCTAGAAAA	240	
QY	1022	TTTGTTTGGATTTTATATCATCTTGTCAAATTGCTTCAGTTGTAATGTGAAAAATGG	1081	
Db	241	TTTGTTTGGATTTTATATCATCTTGTCAAATTGCTTCAGTTGTAATGTGAAAAATGG	300	
QY	1082	GCTGGGAAAGGAGGTGGTGCCCTAAATGTTTACTTGTTAACTTGCTTGTCGCCCT	1141	
Db	301	GCTGGGAAAGGAGGTGGTGCCCTAAATGTTTACTTGTTAACTTGCTTGTCGCCCT	360	
QY	1142	GGGCACATTGGCCTTGTCTGCTCAGTGCTTCCCTTTCACATGGGAAAGGAGTTGTGG	1201	
Db	361	GGGCACATTGGCCTTGTCTGCTCAGTGCTTCCCTTTCACATGGGAAAGGAGTTGTGG	420	
QY	1202	CCAAATCCCAATCTTCTGCACCTCAACGTCGTGGCTCAGGGCTGGGGTGCAGA	1258	
Db	421	CCAAATCCCAATCTTCTGCACCTCAACGTCGTGGCTCAGGGCTGGGGTGCAGA	477	

RESULT 29	
AW050614/c	
LOCUS	AW050614
DEFINITION	w219c10.x1 Soares Dieckgraefe colon_NHCD Homo sapiens linear mRNA 479 bp
	IMAGE:2558514 3', mRNA sequence.
ACCESSION	AW050614
VERSION	AW050614.1
KEYWORDS	EST.
SOURCE	GI:5912884
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 479)
AUTHORS	NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

```

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapps@email.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1432 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 448.
FEATURES
Location/Qualifiers
1..479
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2558514"
/tissue_type="colonic mucosa from 3 patients with Crohn's
disease"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Soares-Dieckgraefe_colon_NHCD"
/notes="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2:Eco RI; 1st

```

strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCCGCTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Tissue samples provided by Dr. Brian Dieckgraefe (Washington University, dieck@im.wustl.edu); colonic mucosa represents a range of disease involvement from moderate to severe Crohn's disease; samples include both perforating (fistulas) and non-perforating samples. Library constructed by Bento Soares and M. Fatima Bonaldo. "		Query Match	31.2%	Score 470;	DB 9;	Length 479;
		Best Local Similarity	100.0%;	Pred. No. 2.2e-149;		
		Matches 470;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1027	TTGAGATTTTATATCATCTTGTCAAAATGCTTCAGTTGTAAATGTGAAAAATGGCGTGG	1086			
Db	470	TTGAGATTTTATATCATCTTGTCAAAATGCTTCAGTTGTAAATGTGAAAAATGGCGTGG	411			
QY	1087	GGAAAGAGGTGGTGCCTTAATGTTTACTTGTAACTTGTTCTTGTCGCCCTCGGCA	1146			
Db	410	GGAAAGAGGTGGTGCCTTAATGTTTACTTGTAACTTGTTCTTGTCGCCCTCGGCA	351			
QY	1147	CTTGGCCCTTGTCTGCCTCAGTGTCTTCCCTTTGACATGGGAAGAGTTGTGGCCAA	1206			
Db	350	CTTGGCCCTTGTCTGCCTCAGTGTCTTCCCTTTGACATGGGAAGAGTTGTGGCCAA	291			
QY	1207	ATCCCATCTTCTTGTGACACCTCAACGCTCTGTGGCTCAGGGCTGGGGTGGCAGAGGGGCC	1266			
Db	290	ATCCCATCTTCTTGTGACACCTCAACGCTCTGTGGCTCAGGGCTGGGGTGGCAGAGGGGCC	231			
QY	1267	TTCACTTATATCTGTGTGTTATCCAGGCTCCAGACTTCCTCTCGCTGCCCACT	1326			
Db	230	TTCACTTATATCTGTGTGTTATCCAGGCTCCAGACTTCCTCTCGCTGCCCACT	171			
QY	1327	GCACCTCTCCCCCTTATCTATCTCCTTCTCGCTCCCCAGCCAGTCTTGGTCTTTGT	1386			
Db	170	GCACCTCTCCCCCTTATCTATCTCCTTCTCGCTCCCCAGCCAGTCTTGGTCTTTGT	111			
QY	1387	CCCTCTCTGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCCAGGGCT	1446			
Db	110	CCCTCTCTGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCCAGGGCT	51			
QY	1447	GGCCCAAGTGGATTTCAATGGTGATCATTAAGAAAGAAAATCGCAACCAA	1496			
Db	50	GGCCCAAGTGGATTTCAATGGTGATCATTAAGAAAGAAAATCGCAACCAA				

RESULT 30
 BM675954/c
 LOCUS
 DEFINITION
 UI-B-EJ0-abf-o-21-0-UI.s1 UI-E-EJ0 Homo sapiens cDNA clone
 UI-B-EJ0-abf-o-21-0-UI 3', mRNA sequence.
 ACCESSION
 BM675954
 VERSION
 BM675954.1 GI:18985850
 SOURCE
 EST.
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 570)
 AUTHORS
 Ronaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL
 Genome Res. 6 (9), 791-806 (1996)
 MEDLINE
 97044477
 PubMed
 8889548
 COMMENT
 Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bentto-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA sequence: 1-38, >POLY_A#Simple_repeat (matched complement)
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
source
1..570
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ0-ahf-o-21-0-UI"
/tissue="UI-E-EJ0-ahf-o-21-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ0"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-EJ0 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTACGGA; eye anterior segment, AATGCCGAT; optic nerve, CCATTAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG TISSUE=human retina TAG LIB=UI-E-EJ0 TAG_SEQ=CCGCG"

ORIGIN
Query Match 31.2%; Score 469; DB 12; Length 570;
Best Local Similarity 100.0%; Pred. No. 4.4e-149; Indels 0; Gaps 0;
Matches 469; Conservative 0; Mismatches 0;

QY 951 GGATTTTAGTGTTGATTTCTGATCAGCGGATACACCTTCCTGTCCACACCCCGACCG 1010
DB 560 GGATTTTAGTGTTGATTTCTGATCAGCGGATACACCTTCCTGTCCACACCCCGACCG 501
QY 1011 GGGCTAGAAAATTTGTTGAGATTTTATATACATCTTGTCATCTGTCAGTTGTAAT 1070
DB 500 GGGCTAGAAAATTTGTTGAGATTTTATATACATCTTGTCATCTGTCAGTTGTAAT 441
QY 1071 GTGAAAATGGGCTGGGAAGGAGTGTCCTAAATTTGTTTACTGTTAACTTGT 1130
DB 440 GTGAAAATGGGCTGGGAAGGAGTGTCCTAAATTTGTTTACTGTTAACTTGT 391
QY 1131 CTTGTGCCCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTGTCCTCCCTTTGACATGGGA 1190
DB 380 CTTGTGCCCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTGTCCTCCCTTTGACATGGGA 321
QY 1191 AGGAGTTGTGGCAAAATCCCATCTTCTTGTGACCTCAAGCTGTGGCTCAGGCTGGG 1250
DB 320 AGGAGTTGTGGCAAAATCCCATCTTCTTGTGACCTCAAGCTGTGGCTCAGGCTGGG 261
QY 1251 GTGCAGAGGGAGGSCCTTCACCTTTATCTGTGTGTTATCCAGGGCTCCAGACTTCCTC 1310

Db 260 GTGCAGAGGGAGGSCCTTCACCTTTATCTGTGTGTTATCCAGGGCTCCAGACTTCCTC 201
QY 1311 CTCTGCTGCCCCCAGCTACGACCTCTCCCTCTATCTATCTCTCTCGCTCCCGAGCC 1370
Db 200 CTCTGCTGCCCCCAGCTACGACCTCTCCCTCTATCTATCTCTCTCGCTCCCGAGCC 141
QY 1371 AGCTTGGCTCTCTGTGCTCCCTCTCGGGGTCACTCCCTCCACTCTGACTCT 1419
Db 140 AGCTTGGCTCTCTGTGCTCCCTCTCGGGGTCACTCCCTCCACTCTGACTCT 92

RESULT 31
BM793929 691 bp mRNA linear EST 05-MAR-2002
LOCUS K-EST0074920 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-32-C08
DEFINITION 5', mRNA sequence.
ACCESSION BM793929
VERSION BM793929.1 GI:19142161
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 691)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
UNPUBLISHED (2002)
CONTACT: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 32 row: C column: 08
High quality sequence stop: 691.
Location/Qualifiers
1..691
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S22SNU16n1-32-C08"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/cell_line="SNU-16"
/lab_host="DH10B"
/clone_lib="S22SNU16n1"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."

ORIGIN
Query Match 30.4%; Score 457; DB 12; Length 691;
Best Local Similarity 100.0%; Pred. No. 4.8e-145; Indels 0; Gaps 0;
Matches 457; Conservative 0; Mismatches 0;

QY 786 GTGTCTCAAAACCGAGATGTGGCCGAGGCTGTTATCTACGTCCTCAGCACCCCGCACA 845
DB 222 GTGTCTCAAAACCGAGATGTGGCCGAGGCTGTTATCTACGTCCTCAGCACCCCGCACA 281
QY 846 CATCCAGATTGGAGACATCCAGATGAGGCCCGAGGAGGTGACCTAGTACTGTGGGA 905
DB 282 CATCCAGATTGGAGACATCCAGATGAGGCCCGAGGAGGTGACCTAGTACTGTGGGA 341

Query Match	30.2%;	Score 455;	DB 10;	Length 455;
Best Local Similarity	100.0%;	Pred. No. 2.7e-144;		

1
2
3
4
5
6

Location/Qualifiers
1 516

FEATURES
source

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-C11-afv-m-21-0-UI"
/tissue_type="RPE and Choroid"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-C11"
/notes="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-C11 is a normalized cDNA library containing the
following tissue(s): RPE and Choroid. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is ACCTA.
This library was created for the program, Gene Discovery
in the Visual System, supported by National Eye Institute
(NEI)."
```

REFERENCE 1 (bases 1 to 886)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@nsl.nsl.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM9753 row: n column: 02
High quality sequence stop: 589.

FEATURES
source
1..886
Location/Qualifiers
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/mol_type="mRNA"
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/clone="IMAGE:3921217"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 30.1%; Score 453; DB 12; Length 516;
Best Local Similarity 100.0%; Pred. No. 1.2e-143;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCGGATCGACCCAGCAGTTCGGCGCGCGGCGGAGGAGCGCGGCGGTTCAGCTCC 60
DB 38 CCGGATCGACCCAGCAGTTCGGCGCGCGGCGGAGGAGCGCGGCGGTTCAGCTCC 97
QY 61 TCGACCCCGCTGTCGGGCTAGTCCAGCGAGCGGCGGCGGCGGCGGCGGCGGCGG 120
DB 98 TCGACCCCGCTGTCGGGCTAGTCCAGCGAGCGGCGGCGGCGGCGGCGGCGGCGG 157
QY 121 CCGGCGATGAGCGGTGGCGGACCGGCTGGGCTGGTGAATGTAAGTGCAGGCTACCCCGGACT 180
DB 158 CCGGCGATGAGCGGTGGCGGACCGGCTGGGCTGGTGAATGTAAGTGCAGGCTACCCCGGACT 217
QY 181 GCGCGGCGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 240
DB 218 GCGCGGCGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 277
QY 241 ACTGTGGGCAACATCGAGGAGTGGCTGCTGTAATGTAAGTGCAGGCTACCCCGGACT 300
DB 278 ACTGTGGGCAACATCGAGGAGTGGCTGCTGTAATGTAAGTGCAGGCTACCCCGGACT 337
QY 301 TTGATCCCTTACAGATGTGACCTATCAATGAAGAGGACATCTCTCCATGTTCTCAGCT 360
DB 338 TTGATCCCTTACAGATGTGACCTATCAATGAAGAGGACATCTCTCCATGTTCTCAGCT 397
QY 361 ATCCGTTCTCAGCAGCGGTGTAGACATCTGATCAACATGCTGGCTTGGCGCGGCGCT 420
DB 398 ATCCGTTCTCAGCAGCGGTGTAGACATCTGATCAACATGCTGGCTTGGCGCGGCGCT 457
QY 421 GACACCCCTGCTCTCAGGCGAGCAGCAGTGGTTGG 453
DB 458 GACACCCCTGCTCTCAGGCGAGCAGCAGTGGTTGG 490

RESULT 34
BE895089
LOCUS 601436007F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3921217 5',
DEFINITION mRNA sequence.
ACCESSION BE895089
VERSION BE895089.1 GI:10358131
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 886)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rgs@nsl.nsl.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM9753 row: n column: 02
High quality sequence stop: 589.

FEATURES
source
1..886
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3921217"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 30.0%; Score 451; DB 10; Length 886;
Best Local Similarity 100.0%; Pred. No. 4.6e-143;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 476 TGCTGGCCCTCAGCATCTGCACACGGGAAGCTACAGTCCATGAAGAGCGGAATGTGG 535
DB 1 TGCTGGCCCTCAGCATCTGCACACGGGAAGCTACAGTCCATGAAGAGCGGAATGTGG 60
QY 536 AGATGGGCGACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTG 595
DB 61 AGATGGGCGACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTG 120
QY 596 TGACCCACTTCTATAGTCCACCAAGTATCGCTCACTCGCTGACAGAGGACTGAGGC 655
DB 121 TGACCCACTTCTATAGTCCACCAAGTATCGCTCACTCGCTGACAGAGGACTGAGGC 180
QY 656 AAGAGCTTGGGAGGCGCCAGACCCACATCCGAGCCACCGTGCATCTCTCCAGGTGTGGTG 715
DB 181 AAGAGCTTGGGAGGCGCCAGACCCACATCCGAGCCACCGTGCATCTCTCCAGGTGTGGTG 240
QY 716 AGACACATTCGCTTCAAACTCCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 775
DB 241 AGACACATTCGCTTCAAACTCCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
QY 776 AGCAATGAAGTGTCTCAAACTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 835
DB 301 AGCAATGAAGTGTCTCAAACTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 836 CCCCCGCGACACATCCAGATTGAGACATCCAGATGAGGCGCCAGGAGGAGGAGGAGGAGGAG 895
DB 361 CCCCCGCGACACATCCAGATTGAGACATCCAGATGAGGCGCCAGGAGGAGGAGGAGGAGGAG 420
QY 896 GACTGTGGGAGTCT 926
DB 421 GACTGTGGGAGTCT 451

RESULT 35
AI673434/c
LOCUS AI673434
DEFINITION w19a10.x1 Soares_Dieckgraefe_colon_NHUC Homo sapiens cDNA clone
IMAGE:2351034 3', mRNA sequence.

```

ACCESSION   AI673434
VERSION     AI673434.1  GI:4853165
KEYWORDS    EST.
SOURCE      Homo sapiens
ORGANISM    Homo sapiens (human)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 481)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE       Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 579 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 457.
FEATURES    source
            1..481
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:2351034"
                /tissue_type="colonic mucosa from 5 ulcerative colitis
                patients"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
                modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
                strand cDNA was primed with a Not I - oligo(dT) primer [5',
                TGTTACCAATCTGAATGGGCGCGCTAGCTTTTCTTTTCTTTT 3'],
                double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not I
                and Eco RI sites of the modified pT73 vector. Library
                went through one round of normalization. Tissue samples
                provided by Dr. Brian Dieckgraefe (Washington University,
                dieck@m.wustl.edu); colonic mucosa represents a range of
                disease involvement from mild cryptitis to severe
                ulceration, fibrosis, and degeneration. Library
                constructed by Bento Soares and M. Fatima Bonaldo. "
```

29.3%; Score 441; DB 9; Length 481;
 Best Local Similarity 100.0%; Pred. No. 1.5e-139;
 Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1055 TGCTTCAGTTGTAATGGAATAATGGGCTGGGAAAGAGGTGGTGTCCTTAATTGTTT 1114
      |||
Db 447 TGCTTCAGTTGTAATGGAATAATGGGCTGGGAAAGAGGTGGTGTCCTTAATTGTTT 388
      |||
QY 1115 TACTTGTAACTTCTTCTTGCCCTGGGCACTTGGCCCTTGTCTGCTCTCAGTGCTT 1174
      |||
Db 387 TACTTGTAACTTCTTCTTGCCCTGGGCACTTGGCCCTTGTCTGCTCTCAGTGCTT 328
      |||
QY 1175 CCCTTTCACATGGGAAGAGGTGTGGCCAAATCCCATCTTCTTGCACTCAACGCT 1234
      |||
Db 327 CCCTTTCACATGGGAAGAGGTGTGGCCAAATCCCATCTTCTTGCACTCAACGCT 268
      |||
QY 1235 GTGGCTCAGGGCTGGGTGGCAGAGGAGGCTTTCACCTTATATCTGTGTGTTATCCAG 1294
      |||
Db 267 GTGGCTCAGGGCTGGGTGGCAGAGGAGGCTTTCACCTTATATCTGTGTGTTATCCAG 208
      |||
QY 1295 GGCTCCAGACTTCTCTCGCTGGCCCTGACCTGACCTCTCCCTTATCTATCTCCTT 1354
      |||
Db 207 GGCTCCAGACTTCTCTCTGCTGGCCCTGACCTGACCTCTCCCTTATCTATCTCCTT 148
      |||
QY 1355 CTCGGCTCCCGAGCCCACTTGTGCTTCTTGTCCCTCTCCCTGATCCCTCCACTCTG 1414
      |||
Db 147 CTCGGCTCCCGAGCCCACTTGTGCTTCTTGTCCCTCTCCCTGATCCCTCCACTCTG 88
      |||
QY 1415 ACTCTGACTATGGCAGCAGAACACCGAGGCTTGGCCAGTGGATTTTCATGGTGCATTA 1474
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Db 87 ACTCTGACTATGGCAGCAGAACACCGAGGCTTGGCCAGTGGATTTTCATGGTGCATTA 28
      |||
QY 1475 AAAAGAGAAAATCGCAACCAA 1495
      |||
Db 27 AAAAGAGAAAATCGCAACCAA 7
      |||
RESULT 36
LOCUS    AI803690/c
DEFINITION tc19e02_x1 Soares NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2064314
            3', mRNA sequence.
ACCESSION AI803690
VERSION   AI803690.1  GI:5369162
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 476)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE       Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 679 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 453.
FEATURES    source
            1..476
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:2064314"
                /tissue_type="Pooled human melanocyte, fetal heart, and
                pregnant uterus"
                /lab_host="DH10B"
                /clone_lib="Soares NhHMPu_S1"
                /note="Organ: mixed (see below); Vector: pT73D-Pac
                (Pharmacia) with a modified polylinker; Site 1: Not I;
                Site 2: Eco RI; Equal amounts of plasmid DNA from three
                normalized libraries (melanocyte 2NbHM, pregnant uterus
                NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                were made in vitro. Following HAP purification, this DNA
                was used as tracer in a subtractive hybridization
                reaction. The driver was PCR-amplified cDNAs from pools of
                5,000 clones made from the same 3 libraries. The pools
                consisted of I.M.A.G.E. clones 260232-265223,
                340488-345479, and 484488-489479."

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29.1%; Score 438; DB 9; Length 476;
 Best Local Similarity 100.0%; Pred. No. 1.6e-138;
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1052 AATTGCTTCAGTTGTAATGGAATAATGGGCTGGGAAAGAGGTGGTGTCCTTAATTG 1111
      |||
Db 438 AATTGCTTCAGTTGTAATGGAATAATGGGCTGGGAAAGAGGTGGTGTCCTTAATTG 379
      |||
QY 1112 TTTTACTTGTAACTTGTCTTGTGCCCCCTGGGCACCTTGGCCCTTGTCTCTCAGTGT 1171
      |||
Db 378 TTTTACTTGTAACTTGTCTTGTGCCCCCTGGGCACCTTGTCTCTCAGTGT 319
      |||
QY 1172 CTTCCCTTTGACATGGGAAAGAGGTGTGGCCAAATCCCATCTTCTTTCACCTCAACG 1231
      |||
Db 318 CTTCCCTTTGACATGGGAAAGAGGTGTGGCCAAATCCCATCTTCTTTCACCTCAACG 259
      |||
QY 1232 TCCTGTGGCTCAGGCTGGGGTGGCAGAGGAGGCTTACCTTATATCTGTGTGTATC 1291
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Db	258	TCTGTGGCTCAGGCTGGGGTGGCAGAGGAGGCGCTTCACTTATATCTGTTGTTATC	199
Qy	1292	CAGGGCTCCAGACTTCTCTCTCTGCTGCCGCCCACTGCACCCCTCTCCCTTATCTATCTC	1351
Db	198	CAGGGCTCCAGACTTCTCTCTCTGCTGCCGCCCACTGCACCCCTCTCCCTTATCTATCTC	139
Qy	1352	CTTCTCGGCTCCAGCCAGCTTGGCTTCTTGTCTCCCTCTGCTGGGTCACTCCCTCCACT	1411
Db	138	CTTCTCGGCTCCAGCCAGCTTGGCTTCTTGTCTCCCTCTGCTGGGTCACTCCCTCCACT	79
Qy	1412	CTGACTCTGACTATGGCAGCAGAACACACAGGCGCTGGCCAGTGGATTTCATGGTATCA	1471
Db	78	CTGACTCTGACTATGGCAGCAGAACACAGGCGCTGGCCAGTGGATTTCATGGTATCA	19
Qy	1472	TTAAAAAGAAAAATCGC	1489
Db	18	TTAAAAAGAAAAATCGC	1
RESULT 37			
LOCUS	BM712008		
DEFINITION	UI-E-EJ0-ahf-o-21-0-UI-r1 UI-E-EJ0 Homo sapiens cDNA clone		
ACCESSION	UI-E-EJ0-ahf-o-21-0-UI 5', mRNA sequence.		
VERSION	BM712008.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 474)		
TITLE	Normalizaton and subtraction: two approaches to facilitate gene discovery		
JOURNAL	Genome Res. 6 (9), 791-806 (1996)		
MEDLINE	97044477		
PUBMED	8889548		
COMMENT	Contact: Soares, MB Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: bento-soares@uiowa.edu Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com). Seq primer: M13 Reverse.		
FEATURES	Location/Qualifiers		
source	1..474		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="UI-E-EJ0-ahf-o-21-0-UI"		
	/tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"		
	/dev_stage="fetal and adult"		
	/lab_host="DHI0B (Life Technologies) ('71 phage resistant)"		
	/clone_lib="UI-E-EJ0"		
	/notes="Organ: eye; Vector: p77T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-EJ0 is a subtraced cDNA library constructed according to Bonaldo, Lennon and Soares. Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p77T3-Pac vector. The oligonucleotide used to prime the synthesis of		
first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAGA; lens, CGATTAGCA; eye anterior segment, AATGCCCAT; optic nerve, CCATTAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."			
ORIGIN			
Query Match	29.0%; Score 437; DB 12; Length 474;		
Best Local Similarity	100.0%; Pred. No. 3.5e-138;		
Matches	437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	951	GGATTTAGGTGTTGATTTCTGGATCAGGGATACCACTTCTCTGCCACACCCCGACAG	1010
Db	1	GGATTTAGGTGTTGATTTCTGGATCAGGGATACCACTTCTCTGCCACACCCCGACAG	60
Qy	1011	GGGCTAGAAAAATTTGTTTGGATTTTATATCATCTTGTCAAAATGCTTCAGTTGTAAT	1070
Db	61	GGGCTAGAAAAATTTGTTTGGATTTTATATCATCTTGTCAAAATGCTTCAGTTGTAAT	120
Qy	1071	GTGAAAAATGGCTGGGGAAAGAGGTGCTGCTCCCTAATGTTTACTTGTAACTTGT	1130
Db	121	GTGAAAAATGGCTGGGGAAAGAGGTGCTGCTCCCTAATGTTTACTTGTAACTTGT	180
Qy	1131	CTTGTGCCCCCTGGGCACCTTGGCTTGTCTCTCAGTGTCTTCCCTTTGACATGGAA	1190
Db	181	CTTGTGCCCCCTGGGCACCTTGGCTTGTCTCTCAGTGTCTTCCCTTTGACATGGAA	240
Qy	1191	AGGAGTTTGGCCAAAATCCCATCTTCTTGCACCTCAACGCTGTGGCTCAGGGCTGG	1250
Db	241	AGGAGTTTGGCCAAAATCCCATCTTCTTGCACCTCAACGCTGTGGCTCAGGGCTGG	300
Qy	1251	GTGGCAGAGGAGGCGCTTACCTTATATCTGTGTTTATCCAGGCTCCAGACTTCTC	1310
Db	301	GTGGCAGAGGAGGCGCTTACCTTATATCTGTGTTTATCCAGGCTCCAGACTTCTC	360
Qy	1311	CTCTGCCCTGCCCACTGCACCTCTCCCTTATCTATCTCTCGGCTCCCGACGCC	1370
Db	361	CTCTGCCCTGCCCACTGCACCTCTCCCTTATCTATCTCTCGGCTCCCGACGCC	420
Qy	1371	AGCTTTGGCTTCTTGTTC	1387
Db	421	AGCTTTGGCTTCTTGTTC	437
RESULT 38			
LOCUS	AI129923/c		
DEFINITION	qc41d08.x1 Soares pregnant uterus_NbHPU Homo sapiens cDNA clone		
ACCESSION	AI129923		
VERSION	AI129923.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 435)		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgaps@mail.nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 670 Std Error: 0.00 Seq primer: -40m13 fwd. RT from Amersham High quality sequence stop: 392.		
FEATURES	Location/Qualifiers		
source	1..435		


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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1712175"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares pregnant uterus NbHPU"
/site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
AAGTGAAGAATTCGGCGCCCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."
```

ORIGIN

```
Query Match      28.9%; Score 435; DB 9; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-137;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1055 TGCTTCAGTTGAATGAAAAATGGCTGGGAAAGAGGTGGTGCCTTAATGTTT 1114
Db      |||
QY 435  TGCTTCAGTTGAATGAAAAATGGCTGGGAAAGAGGTGGTGCCTTAATGTTT 376
Db      |||
QY 1115 TACTGTAACTGTTCTGTGCCCCCTGGGCACTTGGCTTGTCTCAGTGTCTT 1174
Db      |||
QY 375  TACTGTAACTGTTCTGTGCCCCCTGGGCACTTGGCTTGTCTCAGTGTCTT 316
Db      |||
QY 1175 CCCTTTGACATGGGAAGAGGTGTGGCCAAAATCCCATCTCTTGCACTCAACGCT 1234
Db      |||
QY 315  CCCTTTGACATGGGAAGAGGTGTGGCCAAAATCCCATCTCTTGCACTCAACGCT 256
Db      |||
QY 1235 GTGGCTCAGGGCTGGGTGGGAGAGGAGGCTTACCTTATATCTGTGTTTATCCAG 1294
Db      |||
QY 255  GTGGCTCAGGGCTGGGTGGGAGAGGAGGCTTACCTTATATCTGTGTTTATCCAG 196
Db      |||
QY 1295 GGCTCCAGACTTCTCTCTGCTGCCCCCACTGACCTCTCCCGCTTATCTGCTT 1354
Db      |||
QY 195  GGCTCCAGACTTCTCTCTGCTGCCCCCACTGACCTCTCCCGCTTATCTGCTT 136
Db      |||
QY 1355 CTCGGCTCCCCAGCCCCAGCTTGTGCTTCTGCTCCCTCCCTGGGCTCATCTCCACTCTG 1414
Db      |||
QY 135  CTCGGCTCCCCAGCCCCAGCTTGTGCTTCTGCTCCCTCCCTGGGCTCATCTCCACTCTG 76
Db      |||
QY 1415 ACTCTGACTATGGCAGCAGAACACAGGGCTTGCCCAAGTGGATTTCATGATCATTA 1474
Db      |||
QY 75   ACTCTGACTATGGCAGCAGAACACAGGGCTTGCCCAAGTGGATTTCATGATCATTA 16
Db      |||
QY 1475 AAAAAAGAAAAATCGC 1489
Db      |||
QY 15   AAAAAAGAAAAATCGC 1
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RESULT 39
BI765897
LOCUS      804 bp mRNA linear EST 25-SEP-2001
DEFINITION 60346146F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186459 5',
mRNA sequence.
ACCESSION  BI765897
VERSION     BI765897.1 GI:15757475
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 804)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
```

```
Email: c9apbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11465 row: 1 column: 12
High quality sequence stop: 748.
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FEATURES

source

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1..804
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5186459"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned. EcoRV site is
destroyed upon cloning. Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
```

ORIGIN

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Query Match      28.8%; Score 433; DB 12; Length 804;
Best Local Similarity 99.6%; Pred. No. 6.3e-137;
Matches 533; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1   CGCGGATCGGACCCCAAGCAGGTCCGCGCGCGGCGGAGAGCGCGGGCGTCAAGTCC 60
Db      |||
QY 83   CGCGGATCGGACCCCAAGCAGGTCCGCGCGCGGCGGAGAGCGCGGGCGTCAAGTCC 142
Db      |||
QY 61   TCGACCCCGCTGTGCGGCTAGTCCAGCGAGCGGAGCGGCGGCGGCGGCGGCGGCGG 120
Db      |||
QY 143  TCGACTCCCGTGTGCGGCTAGTCCAGCGAGCGGCGGCGGCGGCGGCGGCGGCGG 202
Db      |||
QY 121  CCGCGCATGAGCGGTGGCGCGACCCGCTGCGCTGTGTGACGGGGCGGCTCGGGGGGCA 180
Db      |||
QY 203  CCGCGCATGAGCGGTGGCGCGACCCGCTGCGCTGTGTGACGGGGCGGCTCGGGGGGCA 262
Db      |||
QY 181  GCGCGCGCGCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db      |||
QY 263  GCGCGCGCGCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 322
Db      |||
QY 241  ACTGTGGGCAACATCGAGGAGCTGGCTGTGTAATGTAAGAGTGCAGGCTACCCCGG 300
Db      |||
QY 323  ACTGTGGGCAACATCGAGGAGCTGGCTGTGTAATGTAAGAGTGCAGGCTACCCCGG 382
Db      |||
QY 301  TTGATCCCTACAGATGTGACCTATCAATGAAGAGACATCTCTCTCATGTTCTCAGCT 360
Db      |||
QY 383  TTGATCCCTACAGATGTGACCTATCAATGAAGAGACATCTCTCTCATGTTCTCAGCT 442
Db      |||
QY 361  ATCCGTTCTCAGCAGCGGTGTAGACATCTGATCAACATCTGCTTGGCGCGGCGCT 420
Db      |||
QY 443  ATCCGTTCTCAGCAGCGGTGTAGACATCTGATCAACATCTGCTTGGCGCGGCGCT 502
Db      |||
QY 421  GACACCCCTGCTCTCAGGCGAGCAGCTGGTGTGAAGGACATGTTCAATGTGACGCTG 480
Db      |||
QY 503  GACACCCCTGCTCTCAGGCGAGCAGCTGGTGTGAAGGACATGTTCAATGTGACGCTG 562
Db      |||
QY 481  GCCTCAGCATCTGCACACGGGAAGCTTACCAGTCCATGAAGAGCGGAATGTGG 535
Db      |||
QY 563  GCCTCAGCATCTGCACACGGGAAGCTTACCAGTCCATGAAGAGCGGAATGTGG 617
Db      |||
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RESULT 40

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AA448177/c
LOCUS
DEFINITION
  zW83b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782783
  3', mRNA sequence.
ACCESSION
  AA448177
VERSION
  AA448177.1 GI:2161847
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 430)
  Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
  Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
  Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
  White, Y., Wylie, T., Waterston, R. and Wilson, R.
  WashU-Merck EST Project 1997
  Unpublished (1997)
  Contact: Wilson RK
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  This clone is available royalty-free through LNL; contact the
  IMAGE Consortium (info@image.lnl.gov) for further information.
  Seq primer: -41m13 fwd. ET from Amersham
  High quality sequence stop: 408.
FEATURES
  Location/Qualifiers
    1..430
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:782783"
      /sex="male"
      /lab_host="DH10B"
      /clone_lib="Soares testis NHT"
      /note="Vector: pT73B-Pac (Pharmacia) with a modified
      polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
      was prepared from mRNA obtained from Clontech
      Laboratories, Inc., and primed with a Not I - oligo(dT)
      primer [5',
      TGTTCACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3'].
      Double-stranded cDNA was ligated to Eco RI adaptors
      (Pharmacia), digested with Not I and cloned into the Not I
      and Eco RI sites of the modified pT73 vector. Library
      went through one round of normalization to Cot5, and was
      constructed by Bento Soares and M. Fatima Bonaudo."
ORIGIN
  Query Match 28.4%; Score 428; DB 9; Length 430;
  Best Local Similarity 100.0%; Pred. No. 4.2e-135;
  Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1064 TGTAAATGTGAAATGGCTGGGAAAGAGAGTGTGTCCTAATTTGTTTACTTGTTA 1123
  DB 430 TGTAAATGTGAAATGGCTGGGAAAGAGAGTGTGTCCTAATTTGTTTACTTGTTA 371
  QY 1124 ACTTGTTCTGTGCCCCCTGGGCACITGGCCTTTGTCTGCTCTCAGTGTCTCCCTTGAC 1183
  DB 370 ACTTGTTCTGTGCCCCCTGGGCACITGGCCTTTGTCTGCTCTCAGTGTCTCCCTTGAC 311
  QY 1184 ATGGGAAGAGTTGTGGCCAAATCCCATCTTTCTTGACCTCACTGCTGCTGCTCAG 1243
  DB 310 ATGGGAAGAGTTGTGGCCAAATCCCATCTTTCTTGACCTCACTGCTGCTGCTCAG 251
  QY 1244 GCTGGGGTGGCAGAGGAGGCTTCACTTATATCTGTGTGTATATCCAGGGCTCCAGA 1303
  DB 250 GCTGGGGTGGCAGAGGAGGCTTCACTTATATCTGTGTGTATATCCAGGGCTCCAGA 191
  QY 1304 CTTCCCTCTCTGCTGCCCACTGCACCCCTCTCCCTTATCTATCTCTTCGCTCC 1363
  DB 190 CTTCCCTCTCTGCTGCCCACTGCACCCCTCTCCCTTATCTATCTCTTCGCTCC 131

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QY 1364 CCAGCCAGCTTGGCTTTCTTGTCCTCTCTGGGTTCATCCCTCACTCTGACTCTGACT 1423
DB 130 CCAGCCAGCTTGGCTTTCTTGTCCTCTCTGGGTTCATCCCTCACTCTGACTCTGACT 71
QY 1424 ATGCACAGACACACAGGCGCTGGCCAGTGGATTTTCATGGTGATCATTTAAAAAGAAA 1483
DB 70 ATGCACAGACACACAGGCGCTGGCCAGTGGATTTTCATGGTGATCATTTAAAAAGAAA 11
QY 1484 AATGCGAA 1491
DB 10 AATGCGAA 3

RESULT 41
CB851997/c
LOCUS
DEFINITION
  CB851997 669 bp mRNA linear EST 22-APR-2003
  UI-CF-FNO-aes-e-22-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
  UI-CF-FNO-aes-e-22-0-UI 3', mRNA sequence.
ACCESSION
  CB851997
VERSION
  CB851997.1 GI:30046840
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 669)
  Bonaudo, M.F., Lennon, G. and Soares, M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
  97044477
  8859548
  Contact: McCray, PB
  McCray Lab
  University of Iowa
  2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
  Tel: 319 356 4866
  Fax: 319 356 7171
  Email: paul-mccray@uiowa.edu
  Tissue Procurement: Dr. M. J. Welsh, University of Iowa
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Researchers may obtain clones from Research
  Genetics (www.resgen.com).
  The following repetitive elements were found in this cDNA
  sequence: 1-38, >POLY_A#Simple_repeat (matched complement)
  Seq primer: M13 FORWARD
  POLYA=Yes.
FEATURES
  Location/Qualifiers
    1..669
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="UI-CF-FNO-aes-e-22-0-UI"
      /tissue_type="Human Lung Epithelial cells"
      /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
      /clone_lib="UI-CF-FNO"
      /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
      modified polylinker; Site 1: EcoR I; Site 2: Not I;
      UI-CF-FNO is a subtracted cDNA library derived from two
      normalized Human lung epithelial cell libraries (EN1 and
      DUL) The library was subtracted according to according to
      Bonaudo, Lennon and Soares, Genome Research, 6:791-806,
      1996. For additional information, contact:
      bento-soares@uiowa.edu
      TAG_SEQ=None found"
ORIGIN
  Query Match 28.4%; Score 427; DB 14; Length 669;
  Best Local Similarity 99.7%; Pred. No. 7.4e-135;
  Matches 597; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 907 CTCCTCTTCCCTCCCAACCCCTTCATGGCTTGCTCTGCTCTGATTTTAGTCTTGA 966
Db 604 CTCCTCTTCCCTCCCAACCCCTTCATGGCTTGCTCTGCTCTGATTTTAGTCTTGA 545
QY 967 TTCTCTGATCAGGGATACACTTCTCTCCACCCGACACAGGGGCTAGAAAATTTCG 1026
Db 544 TTCTCTGATCAGGGATACACTTCTCTCCACCCGACACAGGGGCTAGAAAATTTCG 485
QY 1027 TTGAGATTTTATATCATCTTGTCAAATGCTTCAGTTGTAATGTAATAATGGCTGG 1086
Db 484 TTGAGATTTTATATCATCTTGTCAAATGCTTCAGTTGTAATGTAATAATGGCTGG 425
QY 1087 GGAAGAGAGTGGTGTCCCTAAATGTTTACCTTTGTAATGTTCTTGTGCCCCCTGGGCA 1146
Db 424 GGAAGAGAGTGGTGTCCCTAAATGTTTACCTTTGTAATGTTCTTGTGCCCCCTGGGCA 365
QY 1147 CTTGGCCCTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGAAAGGATTTGTGCCAAA 1206
Db 364 CTTGGCCCTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGAAAGGATTTGTGCCAAA 306
QY 1207 ATCCCATCTTCTTGCACTCAACCTCTGTGGCTCAGGGCTGGGTGGCAGAGGAGGCC 1266
Db 305 ATCCCATCTTCTTGCACTCAACCTCTGTGGCTCAGGGCTGGGTGGCAGAGGAGGCC 246
QY 1267 TTCACCTTATATCTGTGTGTATCCAGGGCTCCAGACTTCTCTCTGCTGCCCCCACT 1326
Db 245 TTCACCTTATATCTGTGTGTATCCAGGGCTCCAGACTTCTCTCTGCTGCCCCCACT 186
QY 1327 GCACCCCTCCCTTATCTATCTCTCTCTGCTGCTCCAGCCAGTCTTGTCTTCTTGT 1386
Db 185 GCACCCCTCCCTTATCTATCTCTCTCTGCTGCTCCAGCCAGTCTTGTCTTCTTGT 126
QY 1387 CCCCTCTGGGCTATCCCTCCACTCTGACTCTGACTATGACAGACAGACAGGAGGCC 1446
Db 125 CCCCTCTGGGCTATCCCTCCACTCTGACTCTGACTATGACAGACAGACAGGAGGCC 66
QY 1447 GGCCTAGTGGATTCATGGTGATCATTAAGAAAGAAATCGCAACCAAAAAA 1505
Db 65 GGCCTAGTGGATTCATGGTGATCATTAAGAAAGAAATCGCAACCAAAAAA 7

RESULT 42
BE796469
LOCUS
DEFINITION
601589817f1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943948 5',
mRNA sequence.
ACCESSION
BE796469
VERSION
BE796469.1 GI:10217667
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 1063)
NIH-MGC http://imgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLC800 row: a column: 05
High quality sequence stop: 782.
Location/Qualifiers
1. .1063
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
FEATURES
source

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/clone="IMAGE:3943948"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Query Match 28.2%; Score 425; DB 10; Length 1063;
Best Local Similarity 100.0%; Pred. No. 2.9e-134; Mismatches 0; Indels 0; Gaps 0;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 GACCGCTGGCGCTGGTCAACGGGGGCTCGGGGGGCATCGGGCGCGCTGGCCCGGCC 201
|||||
Db 166 GACCGCTGGCGCTGGTCAACGGGGGCTCGGGGGGCATCGGGCGCGCTGGCCCGGCC 225
|||||
QY 202 CTGCTCCAGCAGGGGACTGAAGGTGGTGGCTCGGCCCGCACTGGGGCAACATCGAGAG 261
|||||
Db 226 CTGCTCCAGCAGGGGACTGAAGGTGGTGGCTCGGCCCGCACTGGGGCAACATCGAGAG 285
|||||
QY 262 CTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGGACTTTGATCCCTACAGATGTAC 321
|||||
Db 286 CTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGGACTTTGATCCCTACAGATGTAC 345
|||||
QY 322 CTATCAATGAAGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGT 381
|||||
Db 346 CTATCAATGAAGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGT 405
|||||
QY 382 GTAGACATCTGCATCAACATGCTGGCTGGCCCGGCTGACACCTGCTCTCAGGAGCAG 441
|||||
Db 406 GTAGACATCTGCATCAACATGCTGGCTGGCCCGGCTGACACCTGCTCTCAGGAGCAG 465
|||||
QY 442 ACCAGTGGTGGAGGACATGTTCAATGTGAACGTGTGGCCCTCAGCATCTGCACACGG 501
|||||
Db 466 ACCAGTGGTGGAGGACATGTTCAATGTGAACGTGTGGCCCTCAGCATCTGCACACGG 525
|||||
QY 502 GAGCCTTACAGTCCATGAAGAGGAGGAGATGTGACGATGGGACATCAATTAACATCAAT 561
|||||
Db 526 GAGCCTTACAGTCCATGAAGAGGAGGAGATGTGACGATGGGACATCAATTAACATCAAT 585
|||||
QY 562 AGCAT 566
Db 586 AGCAT 590

RESULT 43
AW452081/c
LOCUS
DEFINITION
UI-H-B13-ahn-c-06-0-UI.sl NCI_CGAP_Sub5 Homo sapiens cDNA clone
IMAGE:2737163 3', mRNA sequence.
ACCESSION
AW452081
VERSION
AW452081.1 GI:6992857
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 444)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
source
1. .444
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:2737163"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP Sub5"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub5
is a subtracted library derived from NCI CGAP Sub4. The
NCI CGAP Sub5 library had 3 million recombinants. A
single-stranded DNA preparation of NCI CGAP Sub4 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI CGAP Kid3 pool 1 LLAM
3334-3337, 3682-3683, 3798-3803 (IMAGE ClonesIDs
1322376-1323911, 1456008-1456775, 1500552-1502855);
NCI CGAP Kids pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
(IMAGE ClonesIDs 1323912-1325831, 1471368-1472903,
1492104-1493255); NCI CGAP Lu5 pool 1 LLAM 3575-3582,
3851-3854 (IMAGE ClonesIDs
1414920-1417991, 1520904-1522439); NCI CGAP GC4 pool 1 LLAM
3164-3167, 3716-3720, 3733-3735 (IMAGE ClonesIDs
1257096-1258631, 1469064-1470983, 1475592-1476743);
NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068
(IMAGE ClonesIDs 985608-986759, 1101192-1101959,
1217928-1220615); NCI CGAP Co10 pool 1 LLAM 2644-2653,
2871-2872 (IMAGE ClonesIDs
1057416-1061255, 1144584-1145351). (10% of the driver
population), plus a pool of 3,840 arrayed clones from
NCI CGAP Sub1 (IMAGE ClonesIDs 2708616-2710535) and
NCI CGAP Sub2 (IMAGE ClonesIDs 2710536-2712455) (10% of
the driver population), plus a pool of 11,136 clones from
NCI CGAP Sub3 (IMAGE ClonesIDs 2712456-2723591) (10% of the
driver population), plus a pool of 5,472 clones from
NCI CGAP Sub4 (IMAGE ClonesIDs 2723592-2728969) (70% of the
driver population). Subtraction was performed as
previously described [Bonaldo, Lennon & Soares (1996):
Normalization and Subtraction: Two Approaches To
Facilitate Gene Discovery. Genome Research 6, 791-806.
TAG_TISSUE=prostate
TAG_LIB=NCI_CGAP_Pr22
TAG_SEQ=AAGTG"

ORIGIN
Query Match 28.2%; Score 424; DB 10; Length 444;
Best Local Similarity 100.0%; Pred. No. 9, 3e-134;
Matches 42%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1067 AAATGTGAAAAATGGCTGGGAAAGAGGTGGTGCCTTAATGTTTACTGTAACT 1126
DB 444 AAATGTGAAAAATGGCTGGGAAAGAGGTGGTGCCTTAATGTTTACTGTAACT 385
QY 1127 TGTTCCTGTGGCCCTGGGCACATGGCTTGTCTGTCTCAGTGTCTTCCCTTTCATG 1186
DB 384 TGTTCCTGTGGCCCTGGGCACATGGCTTGTCTGTCTCAGTGTCTTCCCTTTCATG 325
QY 1187 GGAAGAGTGTGGGCAAAATCCCATCTTCTTGCACTTCAACGCTGTGGCTCAGGC 1246
DB 324 GGAAGAGTGTGGGCAAAATCCCATCTTCTTGCACTTCAACGCTGTGGCTCAGGC 265
QY 1247 TGGGGTGGCAGAGGAGCCCTTACCTTATCTGTGTTGTTATCCAGGCTCCAGCTT 1306
DB 264 TGGGGTGGCAGAGGAGGAGCCCTTACCTTATCTGTGTTGTTATCCAGGCTCCAGCTT 205
QY 1307 CCTCCTCTGCCCTGCCCTGCACTGCACTCTCTCCCTCTTATCTATCTCTCTCGGCTCCCA 1366

||||| 204 CTTCTCTGCTGCCCTGCCACTGCACCTCTCCCTTATCTCTCTCGGCTCCCA 145
QY 1367 GCCAGTCTTGGCTTCTTGTCCCTCTCTGGGTCATCCCTCCACTCTGACTATG 1426
DB 144 GCCAGTCTTGGCTTCTTGTCCCTCTCTGGGTCATCCCTCCACTCTGACTATG 85
QY 1427 GCAGCAGAACACAGGCGCTGGCCAGTGATTTTCATGTCATTTAAAAAGAAAAAT 1486
DB 84 GCAGCAGAACACAGGCGCTGGCCAGTGATTTTCATGTCATTTAAAAAGAAAAAT 25
QY 1487 CGCA 1490
DB 24 CGCA 21
|||||
RESULT 44
BE869917
LOCUS 601446563F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850574 5',
DEFINITION mRNA sequence.
ACCESSION BE869917
VERSION BE869917.1 GI:10318693
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 614)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9569 row: n column: 15
High quality sequence stop: 602.
Location/Qualifiers
1. 614
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3850574"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 65"
/note="Organ: Colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 Kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 28.1%; Score 423; DB 10; Length 614;
Best Local Similarity 99.8%; Pred. No. 1.8e-133;
Matches 543; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 33 GCAGCAGAGAGCGCGCGCGCTCAGCTCCTCGACCCCGCTGTCGGGTAGTCCAGCAGGC 92
DB 1 GCAGCAGAGAGCGCGCGCGCTCAGCTCCTCGACCCCGCTGTCGGGTAGTCCAGCAGGC 60
QY 93 GCAGCAGCGCGCTGTCGGCCCATGCGCCCGCGCATGCGCGCGCGCTGCGCGCTGCG 152
DB 61 GCAGCAGCGCGCTGTCGGCCCATGCGCCCGCGCATGCGCGCGCGCTGCGCGCTGCG 120
QY 153 GCTGTGTGACGGGGCGCTCGGGGGCGCATCGCGCGCGCGCTGCGCGCGCGCTGCTCCAGCA 212
DB 121 GCTGTGTGACGGGGCGCTCGGGGGCGCATCGCGCGCGCGCTGCGCGCGCGCTGCTCCAGCA 179


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source
1. .751
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4374184"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/notes="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.2 kb and normalized to R0T 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN
Query Match      27.8%; Score 418; DB 10; Length 751;
Best Local Similarity 100.0%; Pred. No. 8e-132;
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGATCGGACCCAAAGCAGGTTCGGCGCGCGCGCAGAGAGCGCGCGGCGTCAGCTCC 60
DB 107 CGCGGATCGGACCCAAAGCAGGTTCGGCGCGCGCGCAGAGAGCGCGCGGCGTCAGCTCC 166

QY 61 TCAGACCCCGTGTTCGGGCTAGTCCAGAGAGCGGACGGCGCGCTGGGCGCCATGCCAGG 120
DB 167 TCAGACCCCGTGTTCGGGCTAGTCCAGAGAGCGGACGGCGCGCTGGGCGCCATGCCAGG 226

QY 121 CCGCGCATGAGCGGTTCGGCGCGACCGCGCTGGCGCTGTGTGACGGGGGGCCTCGGGGGGCATC 180
DB 227 CCGCGCATGAGCGGTTCGGCGCGACCGCGCTGGCGCTGTGTGACGGGGGGCCTCGGGGGGCATC 286

QY 181 GCGCGCGCCGTGGCCCGCGCCCTGGTCCAGCAGGAGCATGAAGGTGGTGGGCTGGCCCGGC 240
DB 287 GCGCGCGCCGTGGCCCGCGCGCCCTGGTCCAGCAGGAGCATGAAGGTGGTGGGCTGGCCCGGC 346

QY 241 ACTGTGGGCAACATCGAGGAGCTGGCTGTCTCAATGTAAGAGTGACAGGCTACCCCGGACT 300
DB 347 ACTGTGGGCAACATCGAGGAGCTGGCTGTCTGAAATGTAGAGTGACAGGCTACCCCGGACT 406

QY 301 TTGATCCCTACAGATGTGACCTATCAAAATGAAGAGGACATCTCTTCCATGTTCTCAGT 360
DB 407 TTGATCCCTACAGATGTGACCTATCAAAATGAAGAGGACATCTCTTCCATGTTCTCAGT 466

QY 361 ATCCGTTCTCAGCACAGGGTGTAGACATCTGCATCAACATGCTGGCTTGGCCCGGC 418
DB 467 ATCCGTTCTCAGCACAGGGTGTAGACATCTGCATCAACATGCTGGCTTGGCCCGGC 524

RESULT 47
BI464353
LOCUS
DEFINITION
603204003F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5269728 5',
mRNA sequence.
ACCESSION
BI464353
VERSION
BI464353.1 GI:15255009
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 757)
NIH-MGC http://imgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
AUTHORS
TITLE
JOURNAL
COMMENT

```

[illegible]

AL568188	2	GI:31291036
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT: Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 8845.f For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF035AG12NP1&cluster=8845.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DF035AG12NP1.		
Location/Qualifiers		
1..980		
/organism="Homo sapiens"		
/mol_type="mRNA"		
/db_xref="taxon:9606"		
/clone="CS0DF035YM23"		
/tissue_type="FETAL BRAIN"		
/dev_stage="fetal"		
/clone_lib="Homo sapiens FETAL BRAIN"		
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."		
Query Match	27.6%	Score 415; DB 9; Length 980;
Best Local Similarity	100.0%	Pred. No. 7.4e-131;
Matches	415; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	925	CCCTTCATCGGTTGCCTCCTGTGGATTATTTAGTGTTGAATTTCTGGATCACGGATA 984
Db	569	CCCTTCATCGGTTGCCTCCTGTGGATTATTTAGTGTTGAATTTCTGGATCACGGATA 510
QY	985	CCACTTCCTGTGCACACCCGCCAGCGGCTAGAAAATTTGTTGAGATTTATATCAT 1044
Db	509	CCACTTCCTGTGCACACCCGCCAGCGGCTAGAAAATTTGTTGAGATTTATATCAT 450
QY	1045	CTTGTCAAATTCCTCAGTTGTAATGTGAAATATGGGCTGGGAAAGGAGTGTTGCC 1104
Db	449	CTTGTCAAATTCCTCAGTTGTAATGTGAAATATGGGCTGGGAAAGGAGTGTTGCC 390
QY	1105	CTAATGTTTTACTTGTTAACTTGTCTTGCCCTCTGGGCACTTGGCCCTTTGTCTGTC 1164
Db	389	CTAATGTTTTACTTGTTAACTTGTCTTGCCCTCTGGGCACTTGGCCCTTTGTCTGTC 330
QY	1165	TCAGTGTCTTCCCTTTGACATGGGAAAGGAGTTGGCCAAATCCCATCTCTTTGCAC 1224
Db	329	TCAGTGTCTTCCCTTTGACATGGGAAAGGAGTTGGCCAAATCCCATCTCTTTGCAC 270
QY	1225	CTCAACGTCGTGGCTCAGGGCTGGGGTGGCAGAGGGCCCTTCACCTTATATCTGTGT 1284
Db	269	CTCAACGTCGTGGCTCAGGGCTGGGGTGGCAGAGGGCCCTTCACCTTATATCTGTGT 210
QY	1285	TGTTATCCAGGGCTCCAGACTTCTCTCTCTGCTGCCCCACATGCACCCTCTCCCC 1339
Db	209	TGTTATCCAGGGCTCCAGACTTCTCTCTCTGCTGCCCCACATGCACCCTCTCCCC 155

RESULT 49		
LOCUS		
DEFINITION		
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 978 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 457.		
Location/Qualifiers		
1..457		
/organism="Homo sapiens"		
/mol_type="mRNA"		
/db_xref="taxon:9606"		
/clone="IMAGE:2558534"		
/tissue_type="colonic mucosa from 3 patients with Crohn's disease"		
/lab_host="DH10B (phage-resistant)"		
/clone_lib="Soares_Dieckgraeefe_colon_NHCD"		
/note="Organ: colon; Vector: pP7TD-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTCGAGCGCGCGCTTTTGTGTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pP7D3 vector. Library went through one round of normalization. Tissue samples provided by Dr. Brian Dieckgraeefe (Washington University, dieck@m.wustl.edu); colonic mucosa represents a range of disease involvement from moderate to severe Crohn's disease; samples include both perforating (fistulas) and non-perforating samples. Library constructed by Bento Soares and M. Fatima Bonaldo."		
Query Match	27.0%	Score 406; DB 9; Length 457;
Best Local Similarity	99.8%	Pred. No. 1.2e-127;
Matches	456; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1037	TATATCATCTTGTCAAATTCGTTTCAGTTGTAAATGTGAAAAATCGCTGGGAAAGGAGG 1096
Db	457	TATATCATCTTGTCAAATTCGTTTCAGTTGTAAATGTGAAAAATCGCTGGGAAAGGAGG 398
QY	1097	TGGTGTCCCTAAATGTTTTACTTGTAACTTGTTCCTGTCGCCCTGGGCATTTGGCCTTT 1156
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QY	1217	TCTTGTCACTCAACGTCGTGGCTCAGGGCTGGGGTGGCAGAGGGAGGCCCTTACCTTAT 1276
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QY	1277	ATCTGTGTGTTATTCAGGGCTCCAGACTTCCTCTCTGCTGCCCCACATGCACCCTCTC 1336
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QY	1337	CCCCCTATATATCTTCCTCGGCTCCCGACCCAGTCTTGGCTTCTTGTCCTCCCTCTGG	1396
Db	157	CCCCCTATATATCTTCCTCGGCTCCCGACCCAGTCTTGGCTTCTTGTCCTCCCTCTGG	98
QY	1397	GGTCATCCCTCCACTCTGACTCTGACTATGCGACAGAACACCCAGGCTGCGCCAGTGG	1456
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Db	37	ATTTTCATGGTGATCATTTAAAGAAAGAAATCGCAACC	1
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ACCESSION	AI378033		
VERSION	AI378033.1	GI:4187886	
KEYWORDS	EST.		
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ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (Bases 1 to 456)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
JOURNAL	Tumor Gene Index		
COMMENT	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	This clone is available royalty-free through LNL; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
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	Equal amounts of plasmid DNA from three normalized		
	libraries (fetal lung NbHL19W, testis NHT, and B-cell		
	NCI CGAP GCBI) were mixed, and ss circles were made in		
	vitro. Following HAP purification, this DNA was used as		
	tracer in a subtractive hybridization reaction. The driver		
	was PCR-amplified cDNAs from pools of 5,000 clones made		
	from the same 3 libraries. The pools consisted of		
	I.M.A.G.E. clones 297480-302087, 682632-687239,		
	726408-728711, and 729096-731399. Subtraction by Bento		
	Soares and M. Fatima Bonaldo. "		

ORIGIN

Query Match	26.9%;	Score 405;	DB 9;	Length 456;
Best Local Similarity	99.8%;	Pred. No. 2.6e-127;		
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QY	1041	TCATCTGTCAATGCTTCAGTGTAAATGTGAAATATGGCTGGGAAAGAGGTGGT	1100	
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QY	1101	GTCCCTAATGTTTACTTGTAACTTGTTCCTGCGCCCTGGGACATTGGCTTTGTCT	1160	
Db	396	GTCCCTAATGTTTACTTGTAACTTGTTCCTGCGCCCTGGGACATTGGCTTTGTCT	337	
QY	1161	GCTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGTGTGGCCAAATCCCATCTTCTT	1220	

Search completed: September 16, 2004, 14:46:12
Job time : 3663 secs

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0116318-A 127 08-MAR-2001; Genentech, Inc. (US)

FEATURES

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ORIGIN

Query Match 100.0%; Score 1505; DB 6; Length 1505; Best Local Similarity 100.0%; Pred. No. 1.5e-278; Indels 0; Gaps 0; Matches 1505; Conservative 0; Mismatches 0;

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Qy 61 TCAGACCCCGGTTCGGGCTAGTCCAGCGAGCGGCGGCGGCGGTTCGGCCCATGGCCAGG 120

Db 61 TCAGACCCCGGTTCGGGCTAGTCCAGCGAGCGGCGGCGGCGGTTCGGCCCATGGCCAGG 120

Qy 121 CCCGCGATGAGCGGTTCGGCGCGGCGGTTCGGCGGTTCGGCGGTTCGGCGGTTCGGCGGT 180

Db 121 CCCGCGATGAGCGGTTCGGCGCGGCGGTTCGGCGGTTCGGCGGTTCGGCGGTTCGGCGGT 180

Qy 181 GCGCGGCGGTTCGGCGGCGGTTCGGCGGCGGTTCGGCGGCGGTTCGGCGGCGGTTCGGCGG 240

Db 181 GCGCGGCGGTTCGGCGGCGGTTCGGCGGCGGTTCGGCGGCGGTTCGGCGGCGGTTCGGCGG 240

Qy 241 ACTGTGGGCAACATCGAGGAGTGGCTGCTGAATGAAGAGGACATCCTCTCCATGTTCTCAGCT 300

Db 241 ACTGTGGGCAACATCGAGGAGTGGCTGCTGAATGAAGAGGACATCCTCTCCATGTTCTCAGCT 300

Qy 301 TTGATCCCTCAGATGTGACCTATCAATGAAGAGGACATCCTCTCCATGTTCTCAGCT 360

Db 301 TTGATCCCTCAGATGTGACCTATCAATGAAGAGGACATCCTCTCCATGTTCTCAGCT 360

Qy 361 ATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACATGCTGGCTTCGGCCCGGCT 420

Db 361 ATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACATGCTGGCTTCGGCCCGGCT 420

Qy 421 GACACCTCTCTCAGGAGCAGCAGTGGTTGGAAGGACATGTTCAATGTGAACGTGCTG 480

Db 421 GACACCTCTCTCAGGAGCAGCAGTGGTTGGAAGGACATGTTCAATGTGAACGTGCTG 480

Qy 481 GCGCTCAGCATCTGCACACGGGAGCCTACAGTCCATGAAGGAGGAAATGGACGAT 540

Db 481 GCGCTCAGCATCTGCACACGGGAGCCTACAGTCCATGAAGGAGGAAATGGACGAT 540

Qy 541 GGGCAGCATATTAACATCAATAGCATGTTCGGCCACCGAGTGTACCCCTGTCTGTGACC 600

Db 541 GGGCAGCATATTAACATCAATAGCATGTTCGGCCACCGAGTGTACCCCTGTCTGTGACC 600

Qy 601 CACTTCTTAGTGCCACCAAGTATCCCTCACTCGCTGACAGGAGGAGTGGAGGAGGAG 660

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Db 781 ATGAGTGTCTCAAAACCGGAGATGTGGCGGAGGCTGTTATCTAGCTCTCAGACCCCC 840

Qy 841 GCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGGAGCGGTGACCTAGTGACTG 900

Db 841 GCACACATCCAGATTGGAGACATCCAGATGAGGCCACGGAGCAGGTGACCTAGTGACTG 900

Qy 901 TGGAGCT 960

Db 901 TGGAGCT 960

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Qy 1141 TGGGCACCTTGGCTTGTCT 1200

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Qy 1201 GCCAAATTCCT 1260

Db 1201 GCCAAATTCCT 1260

Qy 1261 GAGGCTTCACCTTATATCT 1320

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Qy 1321 CCCACTGCACCT 1380

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Db 1501 AAAAA 1505

RESULT 2

AX376310

LOCUS AX376310 1505 bp DNA linear PAT 01-MAR-2002

DEFINITION Sequence 377 from Patent WO0168848.

ACCESSION AX376310

VERSION AX376310.1 GI:19170546

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and Zhang,Z. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0168848-A 377 20-SEP-2001; Genentech, Inc. (US)

FEATURES

source 1..1505 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

ORIGIN

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Qy	181	GGCGCGGCGTGGCGCGGCGGCGTCTGGTCCAGCAGGAGCTGAAAGGTGGTGGGCTGGCGCGGC	240	
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Qy	241	ACTGTGGGCAACATCGAGGAGCTGGCTGTCTGAATGTAAGATGAGAGTACCGCGGACT	300	
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Qy	301	TTGATCCCTACAGATGTGACCTATCAATGAAGAGGACATCTCTCCATGTCTCAGCT	360	
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VERSION	AY358712.1	GI:37182544		
KEYWORDS	FLI CDNA.			
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ORGANISM	Homo sapiens			
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AUTHORS	Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,D., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.			
TITLE	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment			
JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)			
PUBMED	12975309			
REFERENCE	2 (bases 1 to 1505)			
AUTHORS	Clark,H.F.			
TITLE	Direct Submission			
JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA			
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Best Local Similarity	100.0%;	Pred. No. 1.5e-278;		
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Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Butterfield, Y.S., Krywinski, M.I., Skalska, U., Smalish, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 1501)
Strausberg, R.
Direct Submission
Submitted (05-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
On Aug 19, 2003 this sequence version replaced gi:12803782.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.I., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W., Tsurgon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRAL Plate: 12 Row: 9 Column: 18
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AUTHORS Klausner, R.D., Collins, F.S., Wagner, L., Shemen, C.M., Schuler, G.D., Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Altshul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Donald, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wille, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.			
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences			
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)			
MEDLINE 22388257			
PUBMED 12477932			
REFERENCE 2 (bases 1 to 1398)			
AUTHORS Strausberg, R.			
TITLE Direct Submission			
JOURNAL Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov			
COMMENT Contact: MGC help desk			
Email: cgabs-x@mail.nih.gov			
Tissue Procurement: Jeffrey E. Green, M.D.			
cDNA Library Preparation: Life Technologies, Inc.			
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)			
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305			
Web site: http://www-shgc.stanford.edu			
Contact: (Dickson, Mark) mcd@paxil.stanford.edu			
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.			
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov			
Series: IRAK Plate: 25 Row: b Column: 1			
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VERSION AC003042.1 GI:3319121
KEYWORDS HTG.
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ORGANISM Homo sapiens
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REFERENCE 1 (Bases 1 to 102818)
AUTHORS Birren, B., Fasman, K., Linton, L., Nusbaum, C. and Lander, E.
JOURNAL Homo sapiens chromosome 17, clone HCIT75G16
Unpublished
REFERENCE 2 (Bases 1 to 102818)
AUTHORS Birren, B., Fasman, K., McKernan, K., Munro, C., Nusbaum, C.,
Richardson, P., Lander, E., Baldwin, J., Barna, N., Cantu, C., Chang, A.,
Cooke, P., Daly, M. J., Devon, K., Dewar, K., Duret, B., Forrest, C.,
Gage, D., Gensheimer, S., Geraigery, K., Gilman, T., Hags, B.,
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Stillwell, J., Stone, C., Strickland, C., Sydney, K., Tang, L.,
Zentseva, I. and Zody, M.
Direct Submission
Submitted (31-OCT-1997) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (Bases 1 to 102818)
AUTHORS Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatman, C.,
Boutwell, C., Brown, A., Castle, A., Cerny, J., Cooke, P., Depayre, E.,
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Zody, M.
Direct Submission
Submitted (14-JUL-1998) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Jul 14, 1998 this sequence version replaced gi:3294535.
All repeats were identified using RepeatMasker: Smit, A.F.A. &
Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html.
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RESULT 9
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LOCUS
DEFINITION Homo sapiens chromosome 17, clone CTD-2193J24, complete sequence.
ACCESSION AC110594
VERSION AC110594.5 GI:22830329
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 159490)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 17, clone CTD-2193J24
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 159490)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campoliano,A., Chang,J., Chazaro,B.,
Choepeil,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Lacroque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C.,
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Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (13-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 159490)
REFERENCE
AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepeil,Y., Collymore,A.,
Cooke,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (17-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 159490)
REFERENCE
AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepeil,Y., Collymore,A.,
Cooke,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
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Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
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Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
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Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
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Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (13-SEP-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 13, 2002 this sequence version replaced gi:22296745.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L25381
Center clone name: 2193_J_24
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Only the first 159,5 kilobases of this clone are being submitted.
The remainder overlaps accession number AC003042 [WICGR project
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 VERSION AK096551.1 GI:21756072
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K.,
 Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Irie, R.,
 Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J.,
 Isono, Y., Kawai-Hio, Y., Saico, K., Nishikawa, T., Kimura, K.,
 Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H.,
 Kanda, K., Wagatsuna, M., Murakawa, K., Kanehori, K., Sugiyama, A.,
 Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K.,
 and Isogai, T.
 NEDO human cDNA sequencing project
 TITLE NEDO human cDNA sequencing project
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2547)
 AUTHORS Isogai, T. and Yamamoto, J.
 TITLE Direct Submission
 JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
 (E-mail:genomice@hri.co.jp, Tel.81-438-52-3975, Fax:81-438-52-3986)
 Kuzusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
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 Evaluation; clone selection for full insert sequencing: HRI and
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RESULT 12
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 DEFINITION Sequence 109 from Patent WO02098917.
 ACCESSION AX768992
 VERSION AX768992.1 GI:32437160
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Guo, X., Fernandes, E., Li, L., Kekuda, R., Liu, Y., Leite, M.,
 Spyrek, K.A., Ji, W., Casman, S.J., Boldog, F.L., Patturajan, M.,
 Vernet, C.A., Ballinger, R.A., Malyankar, U.M., Tchernev, V.T.,
 Blalock, A.D., Gusev, V.Y., Rastelli, L., Mezes, P.D., Ellerman, K.,
 Heyes, M., Herrmann, J.L., Shimkets, R.A., Toime, N., Pena, C.E.,
 Shenoy, S.G., Taupier, R.J., Gerlach, V. and Gorman, L.
 TITLE Human proteins and nucleic acids encoding same
 JOURNAL Patent: WO 02098917-A 109 12-DEC-2002;
 Curagen Corporation (US)
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RESULT 13
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 DEFINITION Sequence 89 from patent US 6342581.
 ACCESSION AR184145
 VERSION AR184145.1 GI:20228114
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 1 (bases 1 to 569)
 REFERENCE Rosen, C.A., Ruben, S.M., Olsen, H.S. and Ebner, R.
 AUTHORS Secreted protein HHP03
 TITLE Patent: US 6342581-A 89 29-JAN-2002;
 JOURNAL Location/Qualifiers
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Best Local Similarity 99.4%; Pred. No. 2.5e-88;
Matches 535; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

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QY 1388 CCCTCTGGGTGTCATCCCTCCACTCTGACTCTGACTTGGCAGCAGACACAGGGCTG 1447
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QY 1448 GCCCAGTGGATTTTCATGGTGATCATTAATAAAGAAAAATCCCAACCAAAAAA 1505
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ACCESSION         JP 2002513295-A/88.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 569)
Fischer, C.L., Rosen, C.A., Soppet, D.R., Ruben, S.M., Kyaw, H., Li, Y.,
Zeng, Z., Lafleur, D.W., Moore, P.A., Shi, Y., Ols, H.S., Ebner, R. and
Brewer, L.A.
123 human secreted proteins
Patent: JP 2002513295-A 88 08-MAY-2002;
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08-JUL-1997 US 60/051918,08-JUL-1997 US 60/051920 PR
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18-AUG-1997 US 60/055948,18-AUG-1997 US 60/055722 PR

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                    /mol_type="genomic DNA"
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ORIGIN
Query Match      34.1%; Score 513.6; DB 6; Length 569;
Best Local Similarity 99.4%; Pred. No. 2.5e-88;
Matches 535; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

QY 968 TTCTGGATCAGGATACCACTTCTCCCTGCACACCCGACAGGGGCTAGAAAATTTGTT 1027
DB 13 TTCTGGATCAGGATACCA-TCCTGTCMACACCCGACAGGGGCTAGAAAATTTGTT 71

QY 1028 TGAGATTTTATATCATCTTGTCAAAATGCTTCAGTTGTAATGTGAAAATGGCGTGG 1087
DB 72 TGAGATTTTATATCATCTTGTCAAAATGCTTCAGTTGTAATGTGAAAATGGCGTGG 131

QY 1088 GAAAGGAGGTGGTGTCCCTAATTTTACTTTTAACTTCTTGTGCCCTGGGCAC 1147
DB 132 GAAAGGAGGTGGTGTCCCTAATTTTACTTTTAACTTCTTGTGCCCTGGGCAC 191

QY 1148 TTGCCCTTTGTCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAA 1207
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QY 1208 TCCCATCTTTTTCACCTCAACGCTGTGGCTCAGGGCTGGGTGGCAGAGGGAGGCT 1267
DB 252 TCCCATCTTTTTCACCTCAACGCTGTGGCTCAGGGCTGGGTGGCAGAGGGAGGCT 311

QY 1268 TCACCTTATATCTGTGTGTATCCAGGGCTCCAGACTTCCTCTCTGCTGCCCTACTG 1327
DB 312 TCACCTTATATCTGTGTGTATCCAGGGCTCCAGACTTCCTCTCTGCTGCCCTACTG 371

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QY 1388 CCCTCTGGGTGTCATCCCTCCACTCTGACTCTGACTTGGCAGCAGAACACAGGGCTG 1447
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TITLE          1 (bases 1 to 169713)
JOURNAL        Birren,B., Linton,L., Nusbaum,C. and Lander,E.
REFERENCE      Homo sapiens chromosome 17, clone CTD-2047D24
AUTHORS        2 (bases 1 to 169713)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Casle,A., Collinge,M., Collins,S., Collumore,A.,
Cooke,P., DeArrellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,M., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehotzky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wynan,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6446748.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIPR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submission@genome.wi.mit.edu
----- Project Information
Center project name: L855
Center clone name: 2047_D_24
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* NOTE: This record contains 177 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 16, 2004, 16:48:58 ; Search time 2446 Seconds
(without alignments)
3174.230 Million cell updates/sec

Title: US-10-063-735-128
Perfect score: 1337

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Scoring table: BLOSUM62

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Post-processing: Minimum Match 0%
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Listing first 100 summaries

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27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1061	79.4	897	13	BX777216
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10	1025	76.7	932	10	BG030249
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12	983	73.5	612	13	BX671560
13	961	71.9	807	14	CK019037
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39	846	63.3	946	10	BF581815
40	841.5	62.9	748	12	B1761329
41	837	62.6	974	14	CA966917
42	832	62.2	646	9	AL845993
43	824	61.6	672	14	CD469548
44	810	60.6	614	10	BE869917
45	807.5	60.4	977	13	BUS39980
46	801	59.9	567	14	W58472
47	796.5	59.6	763	14	CF348186
48	792	59.2	648	9	AL898132
49	786	58.8	650	14	CD599740
50	785	58.7	863	14	CA474613
51	783	58.6	607	12	BJ624590
52	782	58.5	455	10	BE395404
53	764	57.1	910	14	CF225841
54	763	57.1	650	9	AL895715
55	759	56.8	507	14	W58514
56	748	55.9	545	10	BF076147
57	748	55.9	623	12	BJ005084
58	747	55.9	634	12	BJ528471
59	745	55.7	540	12	BM848396
60	745	55.7	751	10	BG037061
61	737	55.1	736	14	CD494676
62	734	54.9	622	12	BJ502141

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63 734 54.9 632 12 BJ497197
64 732 54.7 654 12 BJ013036
65 731 54.7 633 12 BJ489602
66 730 54.6 609 9 AL646156
67 729.5 54.6 890 14 CA970350
68 723 54.1 704 12 BJ518187
69 718 53.7 809 13 BU090978
70 713 53.3 461 12 BM088288
71 709 53.0 580 14 CA779637
72 707 52.9 686 14 CD496098
73 707 52.9 886 12 BE895089
74 699 52.3 548 12 BM316312
75 695 52.0 755 13 BM187418
76 694 51.9 571 12 BJ521969
77 676 50.6 696 10 BE395162
78 667 49.9 600 9 AL679337
79 653 48.8 547 10 AW640188
80 649 48.5 507 9 AI930229
81 633 47.3 531 9 AI545791
82 633 47.3 639 9 AL877407
83 632 47.3 606 14 CA329988
84 626 46.8 718 12 BU121297
85 624 46.7 516 13 BM708058
86 624 46.7 533 12 BJ014213
87 624 46.7 649 9 AL846856
88 622 46.5 649 12 BJ019121
89 619 46.3 837 13 BM057018
90 618 46.2 453 14 CD734701
91 616 46.1 554 14 BE031247
92 608 45.5 574 14 CF788313
93 607 45.4 663 13 BM307486
94 600 44.9 653 13 BM312777
95 599.5 44.8 1287 13 BU539488
96 598 44.7 871 13 BM128104
97 595 44.5 682 12 BU028379
98 590 44.1 721 12 BJ027323
99 581 43.5 750 13 BM181907
100 577 43.2 742 13 BM179752

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ALIGNMENTS

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BG324477 829 bp mRNA linear EST 27-FEB-2001
6024242421F1 NIH_MGC_14 Homo sapiens CDNA clone IMAGE:4560485 5',
mRNA sequence.

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BG324477 GI:13130914

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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REFERENCE

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AUTHORS

```

```

TITLE

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JOURNAL

```

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COMMENT

```

```

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/BTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Invitae Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1269 row: j column: 06
High quality sequence stop: 755.
Location/Qualifiers
1...829
/organism="Homo sapiens"
/mol_type="mRNA"

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FEATURES
source

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/db_xref="taxon:9606"
/clone="IMAGE:4560485"
/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 14"
/note="Organ: kidney; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

```

Alignment Scores:
Pred. No.: 9,29e-128 Length: 829
Score: 1198.50 Matches: 245
Percent Similarity: 96.86% Conservative: 2
Best Local Similarity: 96.08% Mismatches: 7
Query Match: 89.64% Indels: 4
DB: 12 Gaps: 0
US-10-063-735-128 (1-260) x BG324477 (1-829)
QY 1 MetAlaArgProGlyMetGluArgTrrArgAspArgLeuAlaLeuValThrGlyAlaSer 20
DB 68 ATGGCCAGGCGCGGCGATGGAGCGGTGGCGCGACCGGCTGGTGACCGGGGCGCTCG 127
QY 21 GlyGlyLeuGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
DB 128 GGGGGCATCGCGCGCGCGTGGCGCGGCCCTGGTCCAGCAGGAGGACTGAAGGTGTGGGC 187
QY 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
DB 188 TCGCGCCGCACAGTGGGGCAACATCAGAGAGCTGGTCTGAATGTAAGAGTGCAGGCTAC 247
QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleuSerMet 80
DB 248 CCGGGAGCTTTGATCCCCCTACAGATGTGACCTATCAATGAAGAGGAGCATCTCTCCATG 307
QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
DB 308 TTCTCAGCTATCCGTTCTTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGCTTG 367
QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrrLysAspMetPheAsnVal 120
DB 368 CCGCGGCTGACACCTGCTCTCAGCGAGCACCCAGTGGTGGTGAAGAGCATGTTCAATGTG 427
QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
DB 428 AACGTGTGGCCCTCAGCATCTGCACGCGGAACCTACCACTCCATGAAGAGCGGAAT 487
QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
DB 488 GTGACGATGGGACATCATTAACATCAATAGCATGCTGCGCCACCGAGTGTACCCCTG 547
QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
DB 548 TCTGTGACCCACTTCTATAGTCCCAAGTATGCCGTCTCTGCGCTGACAGAGGAGTGTG 607
QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
DB 608 AGGCAAGAGCTTCGGAGGCGCCAGACCCACATCCAGCCAGCTGATCTCTCCAGGTGTG 667
QY 201 ValGluThr-GlnPheAlaPheLysLeuHisAspLysAspProGlyLysAlaAlaAla 220
DB 668 GTGGAGACCACAATTCGCGCTTCAAACTCCACGACAGGACCCTGAGAAGGAGCATCTGCANC 727
QY 220 rTyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLe 240
DB 728 -TATGAGCAATGAAGTGTCTCAAAACCCGAGGATGTGGCGGAGGCTGTATATACGT-CT 785

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Qy      240 userThrProAlaHisIleGlnIleGlyAspIleGlnMetArg 254
      ||||||| ||||| ||||||| ||||||| ||||| |||||
Db      786 CAGCACCCCGGA-CACATTCGATGGGAGCTCCGATGAAGG 827

RESULT 2
LOCUS   BG741589      822 bp      mRNA      linear      EST 15-MAY-2001
DEFINITION   602635416F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4780659 5',
      mRNA sequence.
ACCESSION   BG741589
VERSION     BG741589.1 GI:14052242
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1. (bases 1 to 822)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10639 row: p column: 04
            High quality sequence stop: 803.

FEATURES             Location/Qualifiers
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                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:4780659"
                    /lab_host="DH10B (T1 phage-resistant)"
                    /clone_lib="NCI_CGAP_Skn3"
                    /note="organ: skin; Vector: pCMV-SPORT6; Site:1: NotI;
                    Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                    Average insert size 1.5kb. Library constructed by Life
                    Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Alignment Scores:
Pred. No.:      2,17e-125      Length:      822
Score:          1178.00      Matches:    234
Percent Similarity: 98.32%      Conservative: 0
Best Local Similarity: 98.32%      Mismatches: 2
Query Match:    88.11%      Indels:      2
DB:             12      Gaps:        0

US-10-063-735-128 (1-260) x BG741589 (1-822)

Qy      1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      102 ATGGCCAGGCCCGGATGGAGCGGTGGCGCGACCGGCTGGCTGGTGCAGGGGGCCCTCG 161

Qy      21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      162 GGGGGCATCGCGCGCGCGTGGCCCGGGCCCTGGTCCAGCAGGAGCTGAGGTGGTGGGC 221

Qy      41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysGlySerAlaGlyTyr 60
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      222 TCGGCCCGCACGTGTGGGCAACATCGAGGAGCTGGCTGCTGAATGTAAAGAGTCAGGCTAC 281

Qy      61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      282 CCCGGAGCTTGCATCCCTACAGATGTGACCTPATCAATGAAGAGGACATCCTCTCCATG 341

Qy      81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

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Db      342 TTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTG 401
Qy      101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      402 GCCCGGCGCTGACACCCCTGCTCTCAGGCAGCACACAGTGGTTGGAGGACATGTTCATATGTG 461
Qy      121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTrpGlnSerMetLysGluArgAsn 140
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      462 AACGTGCTGGCCCTCAGCATCTGCACAGGGAAGCTTACCAGTCTCCATGAAGAGCGGAAT 521
Qy      141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      522 GTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGCCACCGAGTGTATCCCTG 581
Qy      161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      582 TCTGTGACCCACTTCTATAGTGCACCAAGTATGCCGTCACCTGCGCTGACAGAGGACTG 641
Qy      181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      642 AGGCAAGAGCTTCGGAGGAGCCACACATCCAGCCAGCTGTCATCTCCAGGTGTG 701
Qy      201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      702 GTGGAGACACAAATTCGACTTCAAACCTCACGACAGGACCTCGAGAGGAGTGCCACC 761
Qy      221 Tyr-GluGlnMetLys-CysLeuLysProGluAspValAlaGluAlaVal 236
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      762 TATTGAGCAATGAACGTGCTCTCAAAACCGAGGATGTGGCCGAGGCTGTA 811

RESULT 3
LOCUS   BM471232      1010 bp      mRNA      linear      EST 05-FEB-2002
DEFINITION   AGENCOURT_6478395 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5563124
      5', mRNA sequence.
ACCESSION   BM471232
VERSION     BM471232.1 GI:18520274
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1. (bases 1 to 1010)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12293 row: j column: 21
            High quality sequence stop: 561.

FEATURES             Location/Qualifiers
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                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:5563124"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NIH_MGC_72"
                    /note="Organ: skin; Vector: pCMV-SPORT6; Site:1: NotI;
                    Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                    Average insert size 2 kb. Library constructed by Life
                    Technologies."

ORIGIN
Alignment Scores:

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Pred. No.: 3 15e-118 Length: 1010
Score: 1117.50 Matches: 235
Percent Similarity: 91.70% Conservative: 8
Best Local Similarity: 88.68% Mismatches: 15
Query Match: 83.58% Indels: 7
DB: 12 Gaps: 1

US-10-063-735-128 (1-260) x BM471232 (1-1010)

QY 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 87 ATGGCCAGCCCGCGCATGGAGCGGTGGCGCGACCGCGCTGGCTGGTGACGGGGGCTCG 146
QY 21 GlyGlyIleGlyAlaAlaValAlaAlaAlaValGlnGlnGlnGlyLeuValValGly 40
Db 147 GGGGGCATCGGGCGCGCGCTGGCGCGCGCGCGCTGGCTGGTGACGGAGCTGAAGGTGGGGC 206
QY 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 207 TCGCGCCGACCTGTGGCAACATCGAGGAGCTGGCTGAATGTAAGAGTCAGGCTAC 266
QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
Db 267 CCGGGGACTTTGATCCCTACAGATGTGACCTATCAATGAAGAGGACATCTCTCCATG 326
QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
Db 327 TTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGATCAACAAATGCTGCTTG 386
QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal 120
Db 387 GCGCGGCTGACACCTGCTCTCAGGCAGCACACAGTGGTTGGAAGGACATGTTCAATG 446
QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 447 AACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGAAGGCGGAAT 506
QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValIleuProLeu 160
Db 507 GTGGACAGATGGGCATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTATCCCTG 566
QY 161 SerValThrHisPheTyrSerAlaThrTyrValAlaValThrAlaLeuThrGluGlyLeu 180
Db 567 TCTGTGACCCACTTCTATAGTCCACCAAGTATGCCGTCACTGCGCTGCACAGGGGACTG 626
QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 627 AGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCACGTGCTCTCCAGGGGG 686
QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspPro-GluLysAlaAlaAla-T 220
Db 687 GTGGAGACACCATTCGGCTTCAAACTCCCGACCAAGACCTTGGAGAGGAGCTGCCCC 746
QY 220 hrTyrGluGlnMetLysCys-LeuLys-ProGluAspValAlaGluAlaValIleTyr-V 239
Db 747 CCTATGACCAATGAAGTGTCTCCAAACCCCAAGATGGGCCAAGGCTGTATCTACGG 806
QY 239 alLeuSerThrPro---AlaHisIleGlnIleGlyAspIleGlnMetArg-ProThrGlu 257
Db 807 TCTCAGGAACCCCGAACACATTCAGATTGGAAATACTCCCAAAATGAGGGCCCGGAA 866
QY 258 Gln 258
Db 867 CAG 869

RESULT 4
BQ278156
LOCUS
DEFINITION BQ278156 1071 bp mRNA linear EST 07-MAY-2002
AGENCOURT 7061694 NIH_MGC_109 Homo sapiens cDNA clone IMAGE:5805128
5' mRNA sequence.
ACCESSION BQ278156
VERSION BQ278156.1 GI:20488364
KEYWORDS EST.

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1071)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2043 row: n column: 09
High quality sequence stop: 603.
FEATURES
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/clone="IMAGE:5805128"
/tissue_type="teratocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_109"
/note="Organ: ovary; Vector: pOTB7; Site 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dT priming, directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 1 46e-116 Length: 1071
Score: 1103.50 Matches: 230
Percent Similarity: 93.25% Conservative: 5
Best Local Similarity: 91.27% Mismatches: 10
Query Match: 82.54% Indels: 7
DB: 13 Gaps: 3
US-10-063-735-128 (1-260) x BQ278156 (1-1071)
QY 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 96 ATGGCCAGCCCGCGCATGGAGCGGTGGCGCGACCGCGCTGGCTGGTGACGGGGGCTCG 155
QY 21 GlyGlyIleGlyAlaAlaValAlaAlaAlaValGlnGlnGlnGlyLeuLysValValGly 40
Db 156 GGGGCATCGCGCGCGCGCTGGCGCGCGCTGGCTGGTGACGGAGCTGAAGGTGGTGGC 215
QY 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerMetLysTyr 60
Db 216 TCGCGCCGACCTGTGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTCAGGCTAC 275
QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
Db 276 CCGGGGACTTTGATCCCTACAGATGTGACCTATCAATGAAGAGGACATCTCTCCATG 335
QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
Db 336 TTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAAATGCTGGCTG 395
QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal 120
Db 396 GCGCGGCTGACACCTCTCTCAGGAGCAGCAGTGGTGGTGAAGAGACATGTTCAATGTG 455
QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140

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Db      |||||||AACGTGCTGGCCCTCAGCATCTGCACACGGAGAGCCTACAGTCATGAGGAGCGGAAT 515
Qy      |||||||ValAspAspGlyHisIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db      |||||||516 GTGGACGATGGGCACATCATTAACATCAATAGTAGTCTGGCCACCGAGTGTACCCCTG 575
Qy      |||||||161 SerValThrHisPheTyrSerAlaThrIleValThrAlaValThrAlaLeuThrGluGlyLeu 180
Db      |||||||576 TCTGTGACCCACTTCTATAGTGCCACCAAGTAGTCCGCTCAGTCCGCTGACAGAGGAGCTG 635
Qy      |||||||181 ArgGlnGluLeuArgGlu-AlaGlnThrHisIleArgAlaThrCysIleSerProGlyVa 200
Db      |||||||636 AGGCAAGAGCTTCGGAGGGGCCAGACCCACATCCGAGCCAGTGCATCTCTCCAGGTGT 695
Qy      |||||||200 1-ValGluThrGlnPheAlaPheLeuHisAspLysAspPro---GluLysAlaAlaA 219
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Qy      |||||||219 laThrTyrGluGlnMetLysCys-LeuLysProGluAsp-ValAlaGluAlaA---ValIl 237
Db      |||||||756 CCCCCTATGAACAAATGAAGTGTCTCAACCCAAAGGAATGTGGCCCGAAGCTGTGTATC 815
Qy      |||||||237 eTyrValLeu---SerThrProAlaHis 245
Db      |||||||816 TTACGTCTCTTACGACAAACCCCGGCACAC 843

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RESULT 5
 AV654573 651 bp mRNA linear EST 15-JAN-2002
 LOCUS AV654573 GLC Homo sapiens cDNA clone GLCDXC05 3', mRNA sequence.
 DEFINITION AV654573
 ACCESSION AV654573
 VERSION AV654573.1 GI:9875587
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 651)
 Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
 Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
 Shen,K., Lu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
 Hu,G., Gu,J., Chen,Z., and Han,Z.
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 21625106
 11752456
 Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919(ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES
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 1..651
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 /db_xref="taxon:9606"
 /clone="GLCDXC05"
 /tissue_type="corresponding non cancerous liver tissue"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /clone_lib="GLC"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"

Alignment Scores: 1.34e-112 Length: 651

ORIGIN

Pred. No.:
 1.34e-112 Length: 651

Score: 1066.00 Matches: 208
 Percent Similarity: 97.22% Conservative: 2
 Best Local Similarity: 96.30% Mismatches: 6
 Query Match: 79.73% Indels: 0
 DB: 9 Gaps: 0

US-10-063-735-128 (1-260) x AV654573 (1-651)

Qy 11 AspArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAlaAlaValAlaArgAla 30
 Db 2 GACCGCTGGCGCTGGTGCACGGGGGCGCTCGGGGGGCGATCGGGCGCGCTGCCCGGGCC 61
 Qy 31 LeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrValGlyAsnIleGluGlu 50
 Db 62 CTGGTCCAGCAGGAGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCAGGAG 121
 Qy 51 LeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIleProTyrArgCysAsp 70
 Db 122 CTGGCTGCTGAATTAAGAGTGCAGGTACCCCGGACTTTGATCCCTTACAGATGTGAC 181
 Qy 71 LeuSerAsnGluGluAspIleLeuSerMetPheSerAlaIleArgSerGlnHisSerGly 90
 Db 182 CTATCAAAATGAAGAGGACATCTCTCCATGTCTCAGCTATCCGTTCTCAGCACACGCGT 241
 Qy 91 ValAspIleCysIleAsnAsnAlaGlyLeuAlaArgProAsnThrLeuLeuSerGlySer 110
 Db 242 GTAGACATCTGCATCAACAATGTGGCTGGCCCGGCTGACACCTCTCTCAGGCGAGC 301
 Qy 111 ThrSerGlyTyrLysAspMetPheAsnValAsnValLeuAlaLeuSerIleCysThrArg 130
 Db 302 ACCAGTGGTGGAGGACATGTTCAATGTGAACGTGTGGCCCTCAGCATCTGCACACGG 361
 Qy 131 GluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHisIleIleAsnIleAsn 150
 Db 362 GAAGCCTACCACTGCATCAAGAGCGGAATGTGGACCATGGACATGATCAATCAATCAAT 421
 Qy 151 SerMetSerGlyHisArgValLeuProLeuSerValThrHisPheTyrSerAlaThrLys 170
 Db 422 AGCATGTCTGGCCACCGAGTGTATCCCTGTGTGACCCCACTTCTATAGTGCCACCAAG 481
 Qy 171 TyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArgGluAlaGlnThrHis 190
 Db 482 TATGCCGTCATCGCTGCACAGAGGACTGAGGCAAGAGCTTCGAGAGCCCGAGACCCAC 541
 Qy 191 IleArgAlaThrCysIleSerProGlyValValGluThrGlnPheAlaPheLysLeuHis 210
 Db 542 ATCCGAGCCAGTGCATCTCTTCAGGTGGGTGGAGACACAATATCGCTTTAAACTTCAC 601
 Qy 211 AspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLysCys 226
 Db 602 GACAGGGACCTTGAGAGGCGACTGGCAACCTATGAGCAAGGAAGTGC 649

RESULT 6

LOCUS BX777216 897 bp mRNA linear EST 10-DEC-2003
 DEFINITION BX777216 XGC-egg Silurana tropicalis cDNA clone T8gg962g24 3', mRNA sequence.
 ACCESSION BX777216
 VERSION BX777216.1 GI:39684422
 KEYWORDS EST.
 SOURCE Silurana tropicalis (western clawed frog)

ORGANISM

Silurana tropicalis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Silurana.

1 (bases 1 to 897)
 Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
 Sanger Xenopus tropicalis EST project 2001 (11_2003)
 Unpublished (2003)
 Contact: Croning MDR
 Sanger Institute
 Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk

```

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM11444 Row: 1 Column: 14
High quality sequence stop: 781.
Location/Qualifiers
1. .940
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5178397"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/note="Organ: Pooled brain, lung, testis; Vector:
PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27;
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 5,48e-111 Length: 940
Score: 1054.50 Matches: 236
Percent Similarity: 91.01% Conservative: 7
Best Local Similarity: 88.39% Mismatches: 14
Query Match: 78.87% Indels: 11
DB: 12 Gaps: 2

US-10-063-735-128 (1-260) x BI818880 (1-940)

Qy 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeu-ValThrGlyAlaSe 20

```


127 ATGGCAGCCCGCGCATGAGCGGTGGCGCGACCGGCTGGCGCTGTGTGACGGGGCCCTC 186
 QY 20 rGly---GlyIleGlyAlaAlaValAlaArg-AlaLeuValGlnGlnGlyLeuLysValY 39
 Db |||||:::
 187 GGGGTGGCATCTGTGGTGGCGCGGTGGCCCTGGGCCCTGTGTCCAGCAGGAGCTGAAGGTGG 246
 QY 39 aIGlyCysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaG 59
 Db |||||:::
 247 TGGGCTGCCCGCCGCTGTGGCAACATCGAGGAGTGGCTGCTGAATGTAGAGTGCAG 306
 QY 59 lYrProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuS 79
 Db |||||:::
 307 GCTACCCCGGAGCTTGTATCCCTACAGATGTGACCTATCAATGAAGAGGACATCCTCT 366
 QY 79 exMetPheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaG 99
 Db |||||:::
 367 CCATGTTCTCAGCTATCCGTTCTCAGCAGCGGGTGTAGACATCTGCATCAACAATGCTG 426
 QY 99 lYLeuAlaArgProasp-ThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPhe 118
 Db |||||:::
 427 GCTTGGCCCGGCTGACAACTCTCTCAGCAGCAGCAGCAGTGTGTGGAGACATGTTCT 486
 QY 119 Asn-ValAsnVal-LeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysG 138
 Db |||||:::
 487 AATTGTGAACGTTGTGGCCCTCAGCATCTGCACACGGGAAGCCTACCACTCCATGAAGG 546
 QY 138 luArgAsnValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValL 158
 Db |||||:::
 547 AGCGGAATGTGACCATGGGACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGT 606
 QY 158 euProLeuSerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrG 178
 Db |||||:::
 607 TACCCCTGTCTGTGACCCATCTTATAGTGCACCAAGTATCCGCTCAGTCTGACGTGACG 666
 QY 178 luGlyLeuArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCys-IleSer 197
 Db |||||:::
 667 AGGGACTAGGCAAGAGCTTCCGGAGGCCAGCAGCAGATTCGAGCCACGTCGCAATCTCT 726
 QY 198 ProGlyValValGluThr-GlnPheAlaPheLysLeuHisAspLysAspProGluLysAl 217
 Db |||||:::
 727 CAGGTGTGGGGAGACAACTTCGCTTCAAACTCCACGACGAGCCCTTGAGAAGC- 785
 QY 217 aAlaAlaThrTyrGluGlnMetLysCys-LeuLysProGluAspValAlaGluAlaValI 237
 Db |||||:::
 786 -AGTGGCACTATGAGCAATGAAGTGTCTAAACCCGAGGATGTGGCCGAGGCTGTAA 844
 QY 237 leTyrValLeuSerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrG 257
 Db |||||:::
 845 TCTAGCTACTCAGGACC---CTGAACAATCAGATGGAGACATCCAAATTAAGGCCAGGG 901
 QY 257 luGln 258
 Db |||||:::
 902 ACAGG 906
 RESULT 8
 BG967186
 LOCUS
 DEFINITION 602833867F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4988176 5',
 mRNA sequence.
 ACCESSION BG967186
 VERSION BG967186.1 GI:14354823
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 914)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM1000 row: f column: 17
 High quality sequence stop: 748.
 Location/Qualifiers
 1..914
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4988176"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI CGAP Co24"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

FEATURES

source
 Alignment Scores:
 Pred. No.: 1..98e-110 Length: 914
 Score: 1049.50 Matches: 223
 Percent Similarity: 90.15% Conservative: 15
 Best Local Similarity: 84.47% Mismatches: 20
 Query Match: 78.50% Indels: 8
 DB: 12 Gaps: 1
 US-10-063-735-128 (1-260) x BG967186 (1-914)
 QY 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
 Db 105 ATGACTAGAGCTGGCATGGAGCGGTGGCGCGACCGCTGGCACTGGTACGGAGGAGCTCG 164
 QY 21 GlyGlyIleGlyAla-AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValG 40
 Db 165 GGGGGCATCGGTGTGGCTGGCCGTGGCCGGGCATATTAGTCCAGCAGGAGCTGAAGGTTGTGGG 224
 QY 40 YCysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLys-SerAlaGlyT 60
 Db 225 TTGTGCCCGCCGCTGTGGCAACATCGAGAGCTGGCTGCTGATGTAGAGTGCAGGCT 284
 QY 60 YrProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerM 80
 Db 285 ACCCGGGACCTTGATCCCTACAGATGTGACCTGTCAATGAGGAGGACATCTCTTCCA 344
 QY 80 etPheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyL 100
 Db 345 TGTTCTCAGCTGTCCGATCCCGACAGCAGTGGCGTGATATCTGCATCAACAATGCCGCA 404
 QY 100 euAlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnV 120
 Db 405 TGGCCCGGCTGTACACCCCTGTCTCGGCGACACCGAGCGATGGAGGACATGTTCAATG 464
 QY 120 alAsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSer-MetLysGluArg 139
 Db 465 TGAATGTGTGGCCCTCAGCATCTGCATCTGGGAGGCTTATCAGTCCACTCAGCAGGCGG 524
 QY 140 AsnValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuPro 159
 Db 525 AACATAGACGAGCGGCACATCATTAACATCAACAGCATGTGTGGCCACCGAGTCCACCC 584
 QY 160 LeuSerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGly 179
 Db 585 CAGTCTGTGATCCATTTCTATAGTGGGACTAAGTATGCCGTCACTGCACACTGACAGAGGA 644
 QY 180 LeuArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGly 199
 Db 645 CTCAGGCA-GAGCTTCTGGAGGCCAGACCATATCCGGGC-ACGTGTATATCTCTCCAGGC 702

QY 200 Val-ValGluThrGlnPheAlaPheIleuHisLeuAspPro---GluLysAlaAl 218
 Db :::
 703 TTGCGTAGAGACACAGTTCGCTTCAAACTCCATGACAAGGACCCGGGGAACGAGCTG 762
 QY 218 aAlaThrTyTGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValile-T 238
 Db :::
 763 CCCACCTATGATCACTTACCAGTGTCTCAGACACGAGGAGCTGTCTGAGGCTGTCTACT 822
 QY 238 yValLeuSerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluG 258
 Db :::
 823 ACGTGTAGCACAAACCCACATGTCAGGTTGGGACATCCAGATGAGGCCACAGACG 882
 QY 258 ln 258
 Db 883 AG 884

RESULT 9
 BU539642
 LOCUS
 DEFINITION
 AGENCOURT_10224058 NIH_MGC_107 Homo sapiens cDNA clone
 IMAGE:6570429 5', mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC
 cDNA Library Prepared by: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2759 row: e column: 21
 High quality sequence stop: 527.

FEATURES
 source
 1..937
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6570429"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_107"
 /note="Organ: breast; Vector: pOTB7; Site:1: EcoRI;
 Site:2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN
 Alignment Scores:
 Pred. No.: 5,79e-109 Length: 937
 Score: 1037.00 Matches: 216
 Percent Similarity: 90.73% Conservative: 9
 Best Local Similarity: 87.10% Mismatches: 14
 Query Match: 77.56% Indels: 9
 DB: 13 Gaps: 3

US-10-063-735-128 (1-260) x BU539642 (1-937)
 QY 9 TrpArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAlaValAla 28

Db 2 TGGCGGACCGCTGGCGTGGTGACGGGGGCTCGGGGGGCATCGCGCGCGCTGGCC 61
 QY 29 ArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrValGlyAsnIle 48
 Db CGGGCCCTGGTCCAGCAGGACTGAAGGTGGTGGGCTGCGCCGCACTGTGGGCAACATC 121
 QY 49 GluGluLeuAlaAlaGluCysLysSerAlaGlyTyProGlyThrLeuIleProTyArg 68
 Db 122 GAGGAGCTGGCTGCTGAATGTAAGAGTGAGCTACCCCGGACTTTGATCCCTACAGA 181
 QY 69 CysAspLeuSerAsnGluLeuAspIleLeuSerMetPheSerAlaIleArgSerGlnHis 88
 Db 182 TGTGACCTATCAATGAAGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCAC 241
 QY 89 SerGlyValAspIleCysIleAsnAlaGlyLeuAlaArgProAspThrLeuLeuSer 108
 Db 242 AGCGGTGTAGACATCTGCATCAACAATGTGGCTTGGCCCGCTGACACCCCTGCTCTCA 301
 QY 109 GlySerThrSerGlyTrpLysAspMetPheAsnValAsnValLeuAlaLeuSerIleCys 128
 Db 302 GGCAGCACCGAGTGGTTGGAAGGACATGTTCAATGTGAACGTGTGGCCCTCAGCATCTGC 361
 QY 129 ThrArgGluAlaTyrglnSerMetLysGluArgAsnValAspAspGlyHisIleIleAsn 148
 Db 362 ACACGGGAAGCCTACAGTCCATGAAGAGCGGAATGTGACGATGGGCGACATCAATAAC 421
 QY 149 IleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPheTySerAla 168
 Db 422 ATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACCCACTTCTATAGTGC 481
 QY 169 ThrLysTyAlaValThrAlaLeuThrGluGlyLeuArgGlnGlnLeuArgGluAlaGln 188
 Db 482 ACCAAGTATGCCGTCACTCGCTGACAGAGGACTGAGGCAAGAGCTTCGGAGGCCACAG 541
 QY 189 ThrHisIleArgAlaThrCysIleSerProGlyValValGluThrGlnPhe-AlaPheTy 208
 Db 542 ACCACATCCGAGCCACGTCATCTCCAGGTGGGTGGAGACCCCAATTCGCCCTTCCA 601
 QY 208 sIleuHisAsp-LysAspPro---GluLysAlaAlaAlaThrTyGlu-GlnMetLysCys 226
 Db 602 ACTCCACGAAACGAGGACCCCTCGAGAAAGGCTTCTGCCACCCCTATGAACCAATGGAAGTG 661
 QY 227 Leu--LysProGluAspValAlaGluAlaIleTyValLeu-----Ser 241
 Db 662 GTCTCCAAACCCCTAAGAATGTCCCCCGAAGCTTGTATTCTACCTGCCGCCCAAC 721
 QY 242 ThrProAlaHisIleGln 247
 Db 722 CCCCCGAAAAAATCCAG 739

RESULT 10
 BG030249
 LOCUS
 DEFINITION
 602297547F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4392011 5',
 mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Prepared by: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLM10083 row: n column: 12

High quality sequence stop: 601.

Location/Qualifiers

FEATURES

1..932
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:4392011"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dr primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 1,41e-107 Length: 932
Score: 1025.00 Matches: 206
Percent Similarity: 97.18% Conservative: 1
Best Local Similarity: 96.71% Mismatches: 5
Query Match: 76.66% Indels: 2
DB: 10 Gaps: 0

US-10-063-735-128 (1-260) x BG030249 (1-932)

QY 49 GluGluLeuAla-AlaGluCysLysSerAlaGlyTyrProGlyThrLeuLeuProTyrAr 68
DB 1 GAGGAGCTGGCTGCTGATGTAAGAGTCGAGCTACCCGGGACTTTGATCCCTACAG 60
QY 68 gCysAspLeuSerAsnGluAlaAspIleLeuSerMetPheSerAlaIleArgSerGlnHi 88
DB 61 ATGTGACCTATCAATGAAGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGA 120
QY 88 sSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThrLeuLeuSe 108
DB 121 CAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTGGCCGCGCTGACACCTGCTCTC 180
QY 108 rGlySerThrSerGlyTyrLysAspMetPheAsnValAsnValLeuAlaLeuSerIleCy 128
DB 131 AGGCAGCACGAGTGTGAGAGGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTG 240
QY 128 sThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHisIleIleAs 148
DB 241 CACACGGGAAGCTTACCAGTCCATGAAGAGGCGGAATGTGGACGATGGGCACATATTAA 300
QY 148 nIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPheTyrSerAl 168
DB 301 CATCAATAGCATGTCTGGCCACCGAGTGTATCCCTGTCTGTGACCCCACTTCTATAGTC 360
QY 168 aThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArgGluAlaCl 188
DB 361 CACCAAGTATGCGTCACTGCGCTCAGAGGGAGCTGAGGCAAGAGCTTGGGAGGCCCA 420
QY 188 nThrHisIleArgAlaThrCysIleSerProGlyValValGluThrGlnPheAlaPheLy 208
DB 421 GACCCACATCCGAGCCACGTCGATCTCTCCAGTGTGGTGGAGACACAAATTCGCTTCA 480
QY 208 sLeuHisAspLysAspProGluLysAlaAlaThrTyrGluGlnMetLysCysLeuLy 228
DB 481 ACTCCACGACAGGACCCCTGAGAGGCGAGCTGCCACCTATGAGCAAAATGAAGTGTCTCA 540
QY 228 sProGluAspValAlaGluAlaValIleTyrValLeuSerThrProAlaHisIleGlnI 248
DB 541 ACCGAGGATGTGGC-GAGGCTGTATTCTTACGTCTCTCAGCACCCCCCGCACATCCAG 599
QY 248 eGlyAspIleGlnMetArgProThrGluGlnValThr 260
||||| :||| |||||

600 TGGAGACATCAGATGAGGGCCACGAGCAGGTGACC 636

RESULT 11

BE796469

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BE796469 1063 bp mRNA linear EST 20-SEP-2000
601589817F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943948 5',
mRNA sequence.

BE796469.1 GI:10217667

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1063)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLM800 row: a column: 05

High quality sequence stop: 782.

Location/Qualifiers

1..1063

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3943948"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dr priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:
Pred. No.: 4,61e-104 Length: 1063
Score: 995.50 Matches: 225
Percent Similarity: 88.30% Conservative: 9
Best Local Similarity: 84.91% Mismatches: 26
Query Match: 74.46% Indels: 9
DB: 10 Gaps: 1

US-10-063-735-128 (1-260) x BE796469 (1-1063)

QY 1 MetAlaArgProGlyMetGluArgTyrArg-AspArgLeuAlaLeuValThrGlyAlaSe 20
DB 135 ATGGCCAGGCCCGCATGAGCGGTGGCGCTGACCGGTGGCGCTGGTGCAGCGGGGCTC 194
QY 20 rGlyGlyLeGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGl 40
DB 195 GGGGGCATCGCGCGCGCGTGGGCCCGGCTGCTCCAGCAGGAGCTGAAGGTGGTGG 254
QY 40 yCysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTy 60
DB 255 CTGGCCCGGCACTGTGGGCAACATCGAGAGCTGCTGCTGAATGTAAGATGTCAGGCTA 314
QY 60 rProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMe 80
DB 315 CCGGGGACTTTGATCCCTACAGTGTGACCTATCAATGAAGAGGACATCTCTCCAT 374

```

QY      80 tPheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLe 100
Db      375 GTTCTCAGCTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGCTT 434

QY      100 uAlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrTrpLysAspMetPheAsnVa 120
Db      435 GCGCCGGCTGACACCCCTGCTCTCAGGAGACCAAGTGTGGAGGACATGTTCAATGT 494

QY      120 lAsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAs 140
Db      495 GAAACGTGCTGGCCCTCAGCATCTGCACACGGAAGCCTACCAAGTCCATGAAGAGCGGAA 554

QY      140 nValAspAspGlyHisIleIleAsnIleAsnSer-MetSerGlyHisArgValLeuProL 160
Db      555 TGTGACGATGGGCACATCAATTAACATCAATAGCATTTGCTGGCCACCGAGTGTATCCGC 614

QY      160 euSerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGly- 179
Db      615 TGTCTGTGACCAA-TTCTATATGTCAC-AAGTATGCCGTCACTGGCTGACAGAGGAC 672

QY      180 LeuArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIle-SerProGl 199
Db      673 TTGAGGCAAGAGCTTCGGAGGCAAGACCCACATCCGAGCCACGTCGATTTCTCCAGG 732

QY      199 vValValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaL 219
Db      733 TGTGTGGAGACACAAATTCGCTTCAAAAGTCCA-GACAAGGACCTCGAAGGGCAGTGG 791

QY      219 aThrTyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaVal---IleTy 238
Db      792 CAACATATAAGCAATTGAGTGG-TTAAACCCGAGATTTTGCCGAGGATGGAATTAAG 850

QY      238 rValLeuSerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGl 258
Db      851 GGTTCATCAGAAACCCCGCAAGATTCGGAATGCGGAATTCACAATAATGCCACGAGAG 910

QY      258 nValThr 260
Db      911 CCGGACC 917

RESULT 12
LOCUS   BX671560
DEFINITION BX671560 Sus Scrofa library (scac) Sus scrofa cDNA clone
ACCESSION BX671560
VERSION   BX671560.1 GI:37983262
KEYWORDS EST.
SOURCE   Sus scrofa (pig)
ORGANISM Sus scrofa
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S.,
AUTHORS   Soares,M., Bonaldo,P. and Hately,F.
          A Pig Normalised Multi-Tissue cDNA Library
TITLE     Unpublished (2003)
JOURNAL   Contact: Tosser-Klopp G
COMMENT   Institut National de la Recherche Agronomique
          Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
          cedex, FRANCE
          Tel: 33 (0) 5.61.28.51.14
          Fax: 33 (0) 5.61.28.53.08
          Email: tosser@toulouse.inra.fr
          Clone distribution: AGENAE Resource centre, Francois PIUMI,
          Francois.PIUMI@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du
          genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex,
          FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73
          Sequence cleaned of vector, adaptor and repetitions. Contact us
          at signenasupport@jouy.inra.fr to obtain the chromatogram of this
          sequence.

```

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Plate: 0032 row: 1 column: 13.
FEATURES
    source
        1..612
            /organism="Sus scrofa"
            /mol_type="mRNA"
            /db_xref="taxon:9823"
            /clone="scac0032i.1.13"
            /tissue_type="mixed"
            /clone_lib="Sus Scrofa library (scac)"
            /note="Vector: pT73D-pac vector; tissues: adipose tissue,
            brain, kidney, liver, muscle, ovary, testis, heart,
            hypothalamus, pancreas, skin, spleen, thymus, placenta,
            pituitary gland, seminal vesicle, small intestine,
            uterus, adrenals, bulbo urethral gland, cerebral trunk,
            epididymis, female gonad, gall-bladder, hippocampus,
            large intestine, male gonad, melanocytes, stomach, udder"

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ORIGIN

```

Alignment Scores:
Pred. No.:      4,91e-103      Length:      612
Score:          983.00         Matches:    193
Percent Similarity: 97.55%      Conservative: 6
Best local Similarity: 94.61%    Mismatches:  4
Query Match:    73.52%         Indels:      1
DB:             13             Gaps:        0

US-10-063-735-128 (1-260) x BX671560 (1-612)
QY      12 ArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAlaAlaValAlaArgAlaLeu 31
Db      1 CGACTGGCAGCTGGTCACAGGACCTCGGGGGGCATCGCGCGCGCTGCGCCCGGCCCTG 60
QY      32 ValGlnGlnGlyLeuLysValValGlyCysAlaArgThrValGlyAsnIleGluLeu 51
Db      61 GTCCAGCAGCGACTCAAGGTGTGGTGTGTGCCCCCAGCCGCGGGCAACATCGAGGAGCTG 120
QY      52 AlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIleProTyrArgCysAspLeu 71
Db      121 GCGCGCGAGTGTAAAGATGCGAGGCTACCCCGGAGCTTTGATCCCTTACAAATGTGACCTG 180
QY      72 SerAsnGluGluAspIleLeuSerMetPheSerAlaIleArgSerGlnHisSerGlyVal 91
Db      181 TCCAAATGAGGAGGACATCTCTCCATGTTCTCGGCCATCCGCTCTCAACACAGCGGTGTA 240
QY      92 AspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThrLeuLeuSerGlySerThr 111
Db      241 GACATCTGCATCAACAACGCGGGCTTGGCCCGCCGACAGCTGCTCTCAGGCGAGCACC 300
QY      112 SerGlyTyrLysAspMetPheAsnValLeuAlaLeuSerIleCysThrArgGlu 131
Db      301 AGCGGTTGGAGGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACCCGGGAA 360
QY      132 AlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHisIleIleAsnIleAsnSer 151
Db      361 GCCTACCAAGTCCATGAGGAGCGCAAGGTGGATGATGGGCACATCATTAACATCAACAGC 420
QY      152 MetSerGlyHisArgValLeuProLeuSerValThrHisPheTyrSerAlaThrIlySer 171
Db      421 ATGCTGCGCCACCGAGTGTATGTCGCCCATTTTCTATAGTGTACCAAGTAT 480
QY      172 AlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArgGluAlaGlnThrHisIle 191
Db      481 GCCGTCATCGCTGACAGAGGGCTTGAGGAGAGAGCTTCGGGAGGCCAGACCCACATC 540
QY      192 ArgAlaThrCysIleSerProGlyValValGluThrGlnPheAlaPheLysLeu-HisAs 211
Db      541 CGAGCAGCGTGCATCTCTCCAGGAGTCTGTGGAGACACAGATTCGCTTCAAACTCCCATGA 600
QY      211 playspPro 214
Db      601 CCAGAACCC 610

```

RESULT 13

```

CK019037
LOCUS          CK019037      807 bp      mRNA      linear      EST 26-NOV-2003
DEFINITION    AGENCOURT_16543761 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7041546
              5', mRNA sequence.
ACCESSION     CK019037
VERSION       CK019037.1  GI:38544961
KEYWORDS      EST.
SOURCE        Danio rerio (zebrafish)
              Danio rerio
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
              Cypriniformes; Cyprinidae; Danio.
REFERENCE     NIH-MGC http://mgi.nci.nih.gov/
              1 (bases 1 to 807)
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT      Contact: Daniela S. Gerhard, Ph.D.
              Office of Cancer Genomics
              National Cancer Institute / NIH
              Bldg. 31 Rm10A07 Bethesda, MD 20892
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: Len Zon, Harvard
              cDNA Library Preparation: Open Biosystems
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM14798 row: c column: 16
              High quality sequence stop: 686.

FEATURES
    source
        1..807
            /organism="Danio rerio"
            /mol_type="mRNA"
            /db_xref="taxon:7955"
            /clone="IMAGE:7041546"
            /tissue_type="whole body"
            /lab_host="DH10B"
            /clone_lib="NIH_ZGC_10"
            /note="Vector: pExpress1; Site_1: NotI; Site_2: EcoRV;
            Bulk tissue was collected from a whole adult individual
            from the Tuebingen strain. 1st strand cDNA was primed with
            a Not I - oligo(dT) primer, double-stranded cDNA was
            cloned into the Not I and EcoRV sites of pExpress-1.
            Library was size-selected for >1 kb fragments. A
            normalized version of this library is also available
            (NIH_ZGC_7). Library was constructed by Open Biosystems
            (Huntsville, AL)."
```

Alignment Scores:

Pred. No.:	2..81e-100	Length:	807
Score:	961.00	Matches:	178
Percent Similarity:	85.49%	Conservative:	40
Best Local Similarity:	69.80%	Mismatches:	37
Query Match:	71.88%	Indels:	0
DB:	14	Gaps:	0

US-10-063-735-128 (1-260) x CK019037 (1-807)

```

QY      6 MetGluArgTgTpArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyLeuGlyAla 25
Db      12 ATGGATCGCTGGAAGGACAGAGTTCCTTGTCTAGTGGAGCTTCAGTAGGAATAGAGCT 71
QY      26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
Db      72 GCAATCGCAAAAGCTCTTGTCCAGCATGCATGAGAGGTGGTCCGATGTGCCAGAAATGTG 131
QY      46 GlyAsnIleGluGluLeuAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIle 65
Db      132 GAGCAAAATAGAGAAATCGCGCTGAATGTGTCACTGGCGGACTCAGCGGTGTTCTGTTT 191
QY      66 ProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPheSerAlaIleArg 85

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Db      192 CCATATAATGTGATCTTTCAGTAGAGGATGAAGTTTGTCCATGTTCTCTCGGATTAG 251
QY      86 SerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThr 105
Db      252 GCTCAACATAAGGGTGTGATGTGTGATTAATAATGCTGGTTAGCTCTGCCAGAGCCT 311
QY      106 LeuLeuSerGlySerThrSerGlyTropLysAspMetPheAsnValAsnValLeuAlaLeu 125
Db      312 CTTGTTGAACGGCAAGCCAGCGGCTGGAGGACTATGATGAACGTAAGTAAATGTAATGGCCTG 371
QY      126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145
Db      372 GCAGTGTGACCCGCTGAGGCTTACCAGTCCATGAAGAAGAAAGAAATATTGATGATGGCAT 431
QY      146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
Db      432 ATCATTAATATTAAACAGTATGTCTGGCATCGGGTTGTAACAGTCGCTATACACACTTC 491
QY      166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnLeuArg 185
Db      492 TACACCGCTACTAAATACGCAGTGACTCTCTCACCGAAGGTTTCAGGCAAGAGTTACGA 551
QY      186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGlnThrGlnPhe 205
Db      552 GAGGCCAAACCCCATACGTGCGCACAGTATATCCCTGGTTTGTAGTGAGACAGAAATTT 611
QY      206 AlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLys 225
Db      612 GCCTACAGACTCTTTAGTGAACCAACAGACAGGCTTCTGCCACCCTACAAAAGTATAAG 671
QY      226 CysLeuLysProGluAspValAlaGluAlaValIleTyrValLeuSerThrProAlaHis 245
Db      672 TGCTTGCCAGCCAGATGATCTAGCANATGAGTGGTTTATGTCCTAAGCGCTCTCCCTCA 731
QY      246 IleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db      732 TGTTCAATTGGTGACATTCAGATGAGACCTGTGGACAGCTGACA 776

RESULT 14
CF221812
LOCUS      AGENCOURT_1494658 NIH_ZGC_Emb5 Silurana tropicalis cDNA clone
DEFINITION IMAGE:6986808 5', mRNA sequence.
ACCESSION  CF221812
VERSION    CF221812.1  GI:33422520
KEYWORDS   EST.
SOURCE     Silurana tropicalis (western clawed frog)
           Silurana tropicalis
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
           Xenopodinae; Silurana.
REFERENCE  1 (bases 1 to 769)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
           Office of Cancer Genomics
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgapbs-remail.nih.gov
           Tissue Procurement: Robert M. Grainger
           cDNA Library Preparation: Life Technologies, Inc.
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM14656 row: j column: 23
           High quality sequence start: 3
           High quality sequence stop: 711.

FEATURES
    source
        1..769

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/organism="Silurana tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="IMAGE:6986808"
 /tissue_type="gastrula"
 /dev_stage="embryo, stages 10-13"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NICHD_XGC_Emb5"
 /notes="Vector: pCMV-SF0R6.1; Site 1: NotI; Site 2: EcoRV;
 Cloned unidirectionally. Primer: Oligo dt. Average insert
 size 2.0 kb. Constructed by Invitrogen. Note: This is a
 Xenopus Gene Collection (XGC) library."

ORIGIN

Alignment Scores:
 Pred. No.: 9,81e-100 Length: 769
 Score: 956.00 Matches: 182
 Percent Similarity: 89.04% Conservative: 21
 Best Local Similarity: 79.82% Mismatches: 25
 Query Match: 71.50% Indels: 0
 DB: 14 Gaps: 0

US-10-063-735-128 (1-260) x CP221812 (1-769)

QY 6 MetGluArgTTPArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAla 25
 DB 82 ATGGAGCGTGAAGGCGAGGTGGACCTTTGACCGGGCTCGGTGGCATCGAGCC 141
 QY 26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
 DB 142 GCGGTTCGCCGGTCTTGTTCAGCATGTCATGAAGTGGTGGCTGCCAGGCGTT 201
 QY 46 GlyAsnIleGluCluLeuAlaGluCysLysSerAlaGlyTyrProGlyThrIleuLe 65
 DB 202 GATAAGATTTGAAACTGCTGTAATGTGAGAGTGTGGTACCAGGCACCTTATT 261
 QY 66 ProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPheSerAlaIleArg 85
 DB 262 CTTTATAATGTGACCTGTCCTCAATGAAGAGGAGATTCCTCATGTTTTCAGCAATAAG 321
 QY 86 SerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThr 105
 DB 322 ACTTTGCATCAGGGGTCGATGATGATATCAACATGCAGGCTTGGCCGACGGAGCCT 381
 QY 106 LeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnValAsnValLeuAlaLeu 125
 DB 382 TTGCTGAGTGGCAAAACAGAGGATGGAGAACAAATGATTGATTGTTTAAATGTTCTTGCACT 441
 QY 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145
 DB 442 AGTATCTGCACAGAGAGGCTTACCATGTCATGAAGGAAGGAATATCGATGTCCTAT 501
 QY 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
 DB 502 ATCATAAACATCAACAGCATGATGGCCATAGAGTTCTTCTTCTACAGTTATGCACTTT 561
 QY 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
 DB 562 TATTGAGCTACTAAGTATGCTGTAATGCTCCCTGCAGACAGGGCTTCAGGAAGAGTTCAGA 621
 QY 186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGluThrGlnPhe 205
 DB 622 GAAGAAAGAGTCACATCCGAGCAACGAGTATATCCGAGGCTTGTGGAACCTGGATT 681
 QY 206 AlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLys 225
 DB 682 GCATTTAACCTCTTGATATGATCCGGAAGANGCTGTGNCACATATGAAAGTATAAG 741
 QY 226 CysLeuLysProGluAspValAla 233
 DB 742 TGCTGAAAGCTGAGACATTTGCT 765

RESULT 15

BE617298

LOCUS
DEFINITION

BE617298 923 bp mRNA linear EST 20-OCT-2000
 60141804F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846168 5',
 mRNA sequence.

ACCESSION

BE617298

VERSION

BE617298.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 923)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM9558 row: g column: 01
 High quality sequence stop: 698.

FEATURES

source

1..923

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3846168"

/tissue_type="adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 65"

/note="Organ: colon; Vector: pCMV-SF0R6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.8 kb. Library constructed by Life
 Technologies."

ORIGIN

Alignment Scores:

Pred. No.: 1,76e-99 Length: 923

Score: 955.00 Matches: 186

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 71.43% Indels: 0

DB: 10 Gaps: 0

US-10-063-735-128 (1-260) x BE617298 (1-923)

QY 75 GluAspIleLeuSerMetPheSerAlaIleArgSerGlnHisSerGlyValAspIleCys 94
 DB 3 GAGGACATCTCTCCATGTTCTCAGCATTCGTTCTCAGCAGCGGTGTAGACATCTGC 62
 QY 95 IleAsnAsnAlaGlyLeuAlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyr 114
 DB 63 ATCAACAATGCTGGCTTGGCCGGCTGACACCTCTCTCAGGAGCCACCATGTTGG 122
 QY 115 LysAspMetPheAsnValAsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGln 134
 DB 123 AAGGACATGTTCAATGTGAACGTCGTGCCCTCAGCATCTGCACACGGAGACCTACCAG 182
 QY 135 SerMetLysGluArgAsnValAspAspGlyHisIleIleAsnIleAsnSerMetSerGly 154
 DB 183 TCCATGAAGGAGCGGAATGTGACATGGCAGCATCATTAACATCAATAGCATGCTGGC 242
 QY 155 HisArgValLeuProLeuSerValThrHisPheTyrSerAlaThrLysTyrAlaValThr 174
 DB 243 CACCGAGTGTACCCCTGCTGTGACCCACTTCTATAGTGCACCAAGTATGCCGTCAC 302
 QY 175 AlaLeuThrGluGlyLeuArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThr 194

Db 303 GCCTGACAGGAGGACTGAGGCAAGAGCTTCGGGAGGCCCGAGACCACATCCGAGCCACG 362

QY 195 CysIleSerProGlyValValGluThrGlnPheAlaPheIleuHisAspLysAspPro 214

Db 363 TGCATCTCTCCAGGTGTGGGAGACACAAATTCGCTTCAAACTCCACGACAGGACCCCT 422

QY 215 GluLysAlaAlaAlaThrTyrGluGlnMetLysCysLeuLysProGluAspValAlaGlu 234

Db 423 GAGAGGCGAGCTGCCACCTATGAGCAATCAAGTGTCTCAACCCGAGGATGTGGCCGAG 482

QY 235 AlaValIleTyrValLeuSerThrProAlaHisIleGlnIleGlyAspIleGlnMetArg 254

Db 483 GCTGTATCTACTCTCTCAGCAGCCCGCAGCACATCCAGATTGGAGACATCCAGATGAG 542

QY 255 ProThrGluGlnValThr 260

Db 543 CCCACGAGCAGGTGACC 560

RESULT 16

LOCUS BG282361

DEFINITION BG2402863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4545231 5',

ACCESSION BG282361

VERSION BG282361.1 GI:13031288

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 852)

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: c9apbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM1229 row: n column: 16

High quality sequence stop: 851.

FEATURES

source

1..852

Location/Qualifiers

1..852

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4545231"

/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_20"

/note="organ: skin; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:

Pred. No.: 8,67e-99 Length: 852

Score: 948.50 Matches: 206

Percent Similarity: 81.13% Conservative: 9

Best local Similarity: 77.74% Mismatches: 16

Query Match: 70.94% Indels: 34

DB: 12 Gaps: 3

US-10-063-735-128 (1-260) x BG282361 (1-852)

QY 1 MetaAlaProGlyMetGluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSer 20

Db 123 ATGGCCAGGCCCGGATGAGCGGTGGCCGACCGGCTGGCTGGTGGAGCGGGGCTCG 182

QY 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40

Db 183 GGGGGCATCGCGCGGCGGTGGCCGGGCTTGGTCCAGCAGGACTGAAGTGTGGGGC 242

QY 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60

Db 243 TGGCGCCGACATGTGGCAACATCGAGGAGCTGGCTGTAATGTAAAGTGCAGGCTAC 302

QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGlu-GluAspIleLeuSerMe 80

Db 303 CCCGGACTTTGATCCCTTACAGATGTGACCTTATCAAAATGACCGAGGACATCTCTCCAT 362

QY 80 tPheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLe 100

Db 363 GTTCTCAGCTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACATGTGGCTT 422

QY 100 uAlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVa 120

Db 423 GGCCCGGCTGACACCCCTGATCTCAGGCGAGCACCAGTGGTTGGAAGGACATGTTCAATGT 482

QY 120 IAsnVal-LeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgA 140

Db 483 GAACGTGCTTGGCCCTCAGCATCTCACACGGGAAGCCTTACCAGTCCATGAAGGAGCGGA 542

QY 140 snValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProL 160

Db 543 CTGTGAGCATGGGCGACATCATTAACATCAATAGCATGTCTGGACACCGAGTGTACCC 602

QY 160 euSerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyL 180

Db 603 TGCTGTGAACCACTTCTATAGTGCACAAAGTATGCCGTCTACTGCGCTGACAGAGGAC 662

QY 180 euArgGlnLeuArgGluAlaGlnThr-HisIleArgAlaThrCysIle-SerProGl 199

Db 663 TGAGCAAGAGCTTCGGGAGGCCAGCCCAAAATCCGAGCCCAAGTGTCTCCAAACCCCG 722

QY 199 yValValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAla 219

Db 723 AGGAGTGTGGCCGAG---GCTGTAACTACGATCTCAGGAACCC-----GCCAA 770

QY 219 aThrTyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrVa 239

Db 771 CACATTC----- 777

QY 239 lLeuSerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGlu-GlnV 259

Db 778 -----CATATTGGACACATCCAGATGAGGGCCCGCAGGACGAG 815

QY 259 alThr 260

Db 816 TGACC 820

RESULT 17

LOCUS CA474188

DEFINITION IMAGE:6795203 5', mRNA sequence.

ACCESSION CA474188

VERSION CA474188.1 GI:24930540

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 846)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9abbs-remail.nih.gov
Tissue Procurement: Leonard I. Zon, M.D.
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM14304 row: 0 column: 10
High quality sequence stop: 606.
Location/Qualifiers
source
1. 846
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:6795203"
/lab_host="DH10B (T1-resistant)"
/clone_lib="NCI CGAP_ZKId1"
/note="Organ: kidney; Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.8 Kb. Constructed by J. Wang (Research Genetics, Invitrogen Corp) from tissue donated by L. Zon (Harvard University). Note: this is a NCI CGAP Library."

ORIGIN

Alignment Scores:
Pred. No.: 1.67e-98 Length: 846
Score: 946.00 Matches: 181
Percent Similarity: 86.05% Conservative: 41
Best Local Similarity: 70.16% Mismatches: 33
Query Match: 70.76% Indels: 3
DB: 14 Gaps: 0

US-10-063-735-128 (1-260) x CA474188 (1-846)

QY 6 MetGluArgTTPArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyLeuGlyAla 25
Db 16 ATGGATCGCTGGAAGCGCAGAGTGTCTTGTCACCTGGAGCTTCAGTAGAATAGAGCT 75
QY 26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
Db 76 GCAATCGCAAAAGCTCTTGTCCAGCATGCGATGAGTGTTCGATGTCGAGATG 135
QY 46 GlyAsnIleGluGluLeuAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIle 65
Db 136 GAGCAATAGAGAACTGGCGGCTGAATGTGTCAGTGGCGGACTCAGCGGTGCTCTGTTT 195
QY 66 ProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPheSerAlaIleArg 85
Db 196 CCATATAAATGTGATCTTTCAGTAGAGGATGAAGTTTGTCCATGTCCTCGGATTAAG 255
QY 86 SerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThr 105
Db 256 GCTCAACATAAGGGTGTGATGTTTCATTAATATGCTGTTTGTAGCTTCGCCAGAGCT 315
QY 106 LeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnValAsnValLeuAlaLeu 125
Db 316 CTGTTGAACGGCAAAACCAAGCGCTGGAGACTATGATGAACGTGAATGTAATTCGCCCTG 375
QY 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspGlyHis 145
Db 376 GCAGTGTGCACCGTGGCGCTTACCAGTCAUGAAAGAAAGAAATATGATGATGCCAT 435
QY 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
Db 436 ATCATTAATATTAAACAGTATGTCGGGCATCGGGTTGTAAACAGTGCCTATACACTTC 495
QY 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
Db 496 TACACCGCTACTAAATACGAGTGTGCTCTCACCGAAGGTTTGAGCGAAGAGTTACGA 555

QY 186 GluAlaGlnThrHisIleArgAlaThrCysIleSer-ProGlyValValGluThrGlnPh 205
Db 556 GAGGCCAAACCCACCATAGTGGCCACAGTATATCCNCTGGTTAGTGGACAGAAAT 615
QY 205 eAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetly 225
Db 616 TGCCTACAGACTCTTTAGTGAACCAAGACCAAGGCTTCTGCCACTACAAAAGTATAAA 675
QY 225 sCysLeuLysProGluAspValAlaGlu-AlaValIleTyrValLeuSerThrProAlaH 245
Db 676 GTGCCTGACGACAGATGATCTAGCAATGGCAGTGGTTATGCTCTAGCGCTCTCCTC 735
QY 245 IseIleGlnIleGlyAspIleGlnMetArg-ProThrGluGlnValThr 260
Db 736 ATGTTCAAAATGGTGACATTCAGATGAGACCTGTGGACAGCTGACA 783

RESULT 18
CA964199
LOCUS
DEFINITION CA964199 947 bp mRNA linear EST 03-JAN-2003
CCL03a10d20f1 Carp liver library 3 Cyprinus carpio cDNA clone
10d20 5', mRNA sequence.
ACCESSION CA964199
VERSION CA964199.1 GI:27490756
KEYWORDS EST.
SOURCE Cyprinus carpio (common carp)
ORGANISM Cyprinus carpio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprinus.
REFERENCE 1 (bases 1 to 947)
AUTHORS Gracey,A.Y., Fraser,E., Li,W. and Cossins,A.R.
TITLE Microarray and EST analysis of the carp (Cyprinus carpio) transcriptome during environmental stress
JOURNAL Unpublished (2003)
COMMENT Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cossins@liv.ac.uk
Vector has been trimmed from this EST.
Plate: 10 row: d column: 20
Seq primer: TripLex 5' LD (5'-CTCGGAAGCGGCCATTGTGTGT-3')
High quality sequence start: 30
High quality sequence stop: 568.
Location/Qualifiers
source
1. .947
/organism="Cyprinus carpio"
/mol_type="mRNA"
/db_xref="taxon:7962"
/clone="10d20"
/sex="Male & female"
/tissue_type="Liver"
/dev_stage="Adult"
/lab_host="E.coli Electromax DH10B"
/clone_lib="Carp liver library 3"
/note="Vector: pTriplex2; Site 1: SfiI GGCCATTACGGCC;
Site 2: SfiI GGCCGCTCGGCC; Normalized and serially
subtracted cDNA library prepared from liver of warm, cold
and hypoxia challenged animals"

ORIGIN

Alignment Scores:
Pred. No.: 1.31e-97 Length: 947
Score: 939.00 Matches: 173
Percent Similarity: 84.19% Conservative: 40
Best Local Similarity: 68.38% Mismatches: 40
Query Match: 70.23% Indels: 0
DB: 14 Gaps: 0

US-10-063-735-128 (1-260) x CA964199 (1-947)

QY 6 MetGluArgTrrArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAla 25
 Db 58 ATGGATCGCTGGAGAGTGGGTGCTCTGTCTACCTGGAGCTTCACTGGGAATCGGAGCT 117
 QY 26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
 Db 118 GCAATCGCAAGTCTCTCTCCAGCATGCGATGAGGTGATCGCTGCCAGAAATGTG 177
 QY 46 GlyAsnIleGluGluLeuAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIle 65
 Db 178 GAGCAAAATTCAGAAATCGCAGCAGAATGTGTGAGTGGTGAATCAGCGCATCTGATC 237
 QY 66 ProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPheSerAlaIleArg 85
 Db 238 CCGTACAAATGATGATCTGTCTAGAGGACGACATGATATCATGTTCTCTGGATCAA 297
 QY 86 SerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThr 105
 Db 298 GTTCAACATCAGGCGATTCAGCTGTGCAATTAATGCTGTTGGCTCTCCAGAGCT 357
 QY 106 LeuLeuSerGlySerThrSerGlyTrrLysAspMetPheAsnValAsnValLeuAlaLeu 125
 Db 358 CTACTGAGTGGCAAACTAGTGGCTGGAGGACTATGATGATGTAATGTAATGGCTG 417
 QY 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145
 Db 418 TCAGTGTGCACCGCTGAGGCTTACGCTCCATGAAAGAAAGAAATGATGATGTCAT 477
 QY 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
 Db 478 ATCAATTAATATCAACAGATTTGTGACACCGGGTCTCAACCATGCTGATGCACATTC 537
 QY 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
 Db 538 TACAGTGCAGCAAAATATGACGTGACGCTCTCACAGAAAGTTTGAGGCAAGATTACGA 597
 QY 186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGlnThrGlnPhe 205
 Db 598 GAGGCCAAACCCACATAGTCCACATGATTTCTCTGGTTAGTGAGACAGAAATT 657
 QY 206 AlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLys 225
 Db 658 GCCTACCGACTCTTTAGCGNAACCCAGAAATAGCTGTGCTACCTACACNAGTGTAAAG 717
 QY 226 CysLeuLysProGluAspValAlaGluAlaValIleTyrValLeuSerThrProAlaHis 245
 Db 718 TGCCCTACNAGCAGTTGACATCGCAAACTCAGTGGTGTATGCTCCTGAGTCTCTCTCAT 777
 QY 246 IleGlnIleGlyAspIleGlnMetArgProThrGlnGln 258
 Db 778 GNTCAATGGGTGACATTGAGATCACCAGCTGGAGCAG 816
 RESULT 19
 LOCUS CA969358
 DEFINITION CckX06a22g15f1 Carp mixed tissue library 3 Cyprinus carpio cDNA
 clone 22g15 5', mRNA sequence.
 ACCESSION CA969358
 VERSION 1
 KEYWORDS EST.
 SOURCE Cyprinus carpio (common carp)
 ORGANISM Cyprinus carpio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Cyprinus.
 1 (bases 1 to 819)
 AUTHORS Gracey A.Y., Fraser E., Li W. and Cossins A.R.
 TITLE Microarray and EST analysis of the carp (Cyprinus carpio)
 transcriptome during environmental stress
 JOURNAL Unpublished (2003)
 COMMENT Contact: Andrew R. Cossins
 Laboratory for Environmental Gene Regulation

University of Liverpool
 School of Biological Sciences, The Biosciences Building, Crown
 Street, Liverpool, United Kingdom, L69 7ZB
 Tel: +44(0)151-795-4510
 Fax: +44(0)151-795-4431
 Email: cossins@liv.ac.uk
 Vector has been trimmed from this EST.
 Plate: 22 row: 9 column: 15
 Seq primer: TripLex 5' LD (5'-CTCGGGAAGCGCCATGTGTGTGT-3')
 High quality sequence start: 65
 High quality sequence stop: 569.

FEATURES

Location/Qualifiers
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 /organism="Cyprinus carpio"
 /mol_type="mRNA"
 /db_xref="taxon:7962"
 /clone="22g15"
 /sex="Male & female"
 /tissue_type="Skeletal white muscle, cardiac muscle,
 kidney, brain, gill, intestinal mucosa"
 /dev_stage="Adult"
 /lab_host="E.coli Electromax DH10B"
 /clone_lib="Carp mixed tissue library 3"
 /note="Vector: pTriplex2; Site_1: SfiI GGCCATTACGGCC;
 Site_2: SfiI GGCGCTCGGCC; Normalized and serially
 subtracted cDNA library prepared from mixed tissues of
 warm, cold and hypoxia challenged animals"

ORIGIN

Alignment Scores:
 Pred. No.: 2,96e-97 Length: 819
 Score: 935.00 Matches: 173
 Percent Similarity: 84.92% Conservative: 41
 Best Local Similarity: 68.65% Mismatches: 38
 Query Match: 69.93% Indels: 0
 DB: 14 Gaps: 0
 US-10-063-735-128 (1-260) x CA969358 (1-819)
 QY 6 MetGluArgTrrArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAla 25
 Db 59 ATGGTCCGCTGAAAGGCGAGGCTTGCTCTGTCTACCTGGAGCTTCACTGGGAATCGGAGCT 118
 QY 26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
 Db 119 GCAATCCCAAGTCTCTTGTCCAGCATGCGATGAAAGTGGGGGCTGTGCCAAAAATGTG 178
 QY 46 GlyAsnIleGluGluLeuAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIle 65
 Db 179 GGGCAATTAAGAAATTCGCTGCTGAATGTCTAGTAGTGAATCAGCGGCACTCTGATA 238
 QY 66 ProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPheSerAlaIleArg 85
 Db 239 CCATATAAATGTGATCTCTCTGTAAGGACGACATGTTATCCATGTTCTCTCTGGATCAA 298
 QY 86 SerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThr 105
 Db 299 GTTCAACATCAGGAGATTGACGTGTGCAATTAATAATGCTGTTGGCTCTCCCTCGCCT 358
 QY 106 LeuLeuSerGlySerThrSerGlyTrrLysAspMetPheAsnValAsnValLeuAlaLeu 125
 Db 359 CTATTGACGGCGGAACCACTGGCTGGAGGACTATGATGATGATGCAATGTCTATGGGCTG 418
 QY 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145
 Db 419 TCAGTGTGACCCGCTGAGGCATACCATCTCCATGAAGAACCAATATTGATGATGGTTCAT 478
 QY 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
 Db 479 ATCATTAAATTAACAGCATGAGTGGACACCGGGTCGTCACCAATGCGCATGTACATTC 538
 QY 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
 Db 538 TACAGTGCAGCAAAATATGACGTGACGCTCTCACAGAAAGTTTGAGGCAAGATTACGA 597

Db 539 TACAGTGTACCAATATGACAGCTCTCACACAGGTTTGAGGCAAGAGTTACAA 598
 QY 186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGluThrGlnPhe 205
 Db 599 GAGGCCAAAACCCACATACAGGACCATGTAATTTCTCTGTTTAGTGAGAGACAGAAATTT 658
 QY 206 AlaPheLysLeuHisAspLysAspProGluLysAlaAlaThrThrGluGlnMetLys 225
 Db 659 GCGTACCGACTCTTAAGTGAACACCCAGAAAGGCTGCTGCTACTTATATAAGATATAAG 718
 QY 226 CysLeuLysProGluAspValAlaGluAlaValIleThrValLeuSerThrProAlaHis 245
 Db 719 TCCTTCAGAGCATGACATCNCAACGCCANGGTGTGCTCTGAGTGCTCTCTCAT 778
 QY 246 IleGlnIleGlyAspIleGlnMetArgProThrGlu 257
 Db 779 GTCTCAATTTGGTGACATTCAGATGAAGCCGTGGAG 814

RESULT 20
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 LOCUS 602024015F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4159658 5',
 DEFINITION mRNA sequence.
 ACCESSION BF233600
 VERSION BF233600.1 GI:11144177
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 881)
 AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-rc@mail.nih.gov
 Tissue procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLN9437 row: m column: 03
 High quality sequence stop: 764.

FEATURES

Source
 1. .881
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4159658"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Li9"
 /notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Alignment Scores:
 Pred. No.: 3 84e-97 Length: 881
 Score: 934.50 Matches: 209
 Percent Similarity: 89.17% Conservative: 5
 Best Local Similarity: 87.08% Mismatches: 20
 Query Match: 69.90% Indels: 9
 DB: 10 Gaps: 1

US-10-063-735-128 (1-260) x BF233600 (1-881)

QY 1 MetaLArgProGlyMetGluAlaThrArgAspArgLeuAlaLeuValThrGlyAlaSer 20
 Db 112 ATGACTAGAGCTGGCATGGAGCGGTGGCGCGACCGCTGCTGAGCGGAGCGCTCG 171

QY 21 GlyGlyIleGlyAlaAlaValAlaAlaLeuValGln-GinglyLeuLysValValGI 40
 Db 172 GGGGGCATCGGTGGCGCGGTGGCCGGGCATTAGTCCAGTCAGGAGCTGAAGTGTGGG 231
 QY 40 yCysAlaArgThrValGlyAsnIleGluGlu-LeuAlaAlaGluCysLysSerAlaGlyT 60
 Db 232 TTGTGCCCGCACCGTTGGCAACATCGAGGAGACTGGCTGCTGAATGTAGAGTGCAGGCT 291
 QY 60 yProGlyThrLeuIleProTyraGcysAspLeuSerAsnGluGluAspIleLeuSerM 80
 Db 292 ACCCGGGGACTTGTATCCCTACAGATGTACCTGTCAAAATGAGGAGGACATCTCTCCA 351
 QY 80 etPheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAenAsnAlaGlyL 100
 Db 352 TGTTCTAGCTGTCGATCCCGACAGCAGTGGCGTGATATCTGCATCAACAATGCCGGA 411
 QY 100 euAlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnV 120
 Db 412 TGGCCCGGCTGACACCCCTGCTCTCGGCAGCACCCAGCGGATGGAAGGACATGTTCAATG 471
 QY 120 alaSnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgA 140
 Db 472 TGAATGTGTGGCCCTCAGCATCTGCATCTGGGAGGCTTATCAGTCCATGAAGAGCGGA 531
 QY 140 snValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProL 160
 Db 532 ACATAGACACCGGGCACATCATTAACATCAACAGCATGTGGCCACCCAGGCCACCCC 591
 QY 160 euSerValThrHisPheTyrSerAlaThrLysTyr-AlaValThrAlaLeuThrGlu-Gl 179
 Db 592 AGTCTGTGATCCATTCTATAGTGGACTAAGTAATTCGCGTCAGCTGACTGCAGAGGGG 651
 QY 179 yLeuArgGlnGluLeuArgGluAlaGlnThrHisIleArg-AlaThrCysIleSerProG 199
 Db 652 ACTCAGGCAAGAGCTTCTGGAGGC-CAGACCCATATTCGGGGCCACGTGTATCTCTCCAG 710
 QY 199 lyValValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAla 219
 Db 711 GTTGTGTAGACACAGTTCGGCTTCAAACT-CATGACAACGTACCCTGGGAGAGAGCTG 769
 QY 219 laThrTyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAla 235
 Db 770 CACTATGAACACCT---AGTGTTCACACCAAG-GACGTGGCTGAGGCT 815

RESULT 21
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 LOCUS K-EST0017362 S1SNU5s1 Homo sapiens cDNA clone S1SNU5s1-4-C01 5',
 DEFINITION mRNA sequence.
 ACCESSION BM744024
 VERSION BM744024.1 GI:19065353
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 566)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 4 row: C column: 01
 High quality sequence stop: 566.
 Location/Qualifiers

FEATURES

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source
1. .566
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/sex="F"
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/cell_type="Lymphoblast-like"
/lab_host="Top10F"
/clone_lib="S1SNU5s1"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dt)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the substracted cDNA libraries were constructed by transformatioin of the remaining DNA into competent cells E. coli Top10F with electroporation method."

ORIGIN

Alignment Scores:
Pred. No.: 1,31e-96 Length: 566
Score: 927.00 Matches: 180
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.33% Indels: 0
DB: 12 Gaps: 0

US-10-063-735-128 (1-260) x BM744024 (1-566)

QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
Db 3 TTCTCAGTATCCGTTCTCAGCACACGCGGTGTAGACATCTGCATCAACAATCTGGCTTG 62
QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAsnMetPheAsnVal 120
Db 63 GCCCGCCTTGACACCTCTCTCAGCAGCACCGATGGTGTGGAGGACATGTTCATGTG 122
QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetIysGluArgAsn 140
Db 123 AACGTGTGGCCTTCAGCATCTGCACACGGGAAGCTACCATCTCCATGAGAGCGGAAT 182
QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 183 GTGGACGATGGGCACATCAATTAACATCAATGATGTCTGGCCACCGAGTGTACCCCTG 242
QY 161 SerValThrHisPheThrSerAlaThrIlystTyrAlaValThrAlaIleuThrGluGlyLeu 180
Db 243 TCTGTGACCACTTCTATAGTCCCAAGTAATGCGTGCCTGACTGCGCTGACAGAGGACTG 302
QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200

```

```

Db 303 AGGCAAGAGCTTCGGAGGCCAGCCACATCCGAGCCACGTCATCTCTCCAGGTGTG 362
QY 201 ValGluThrGlnPheAlaPheTysLeuHisAspLysAspProGluLysAlaAlaIaThr 220
Db 363 GTGGAGACACAATTCGCTTCAAACTCCACGACAAGACCTTGAGAAGCGAGTGCACC 422
QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 423 TATGACCAATGAAGTGTCTCAAAACCCGAGGATGTGCCCGAGGCTGTATCTACGTCCTC 482
QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 483 AGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGGAGTGACC 542

RESULT 22
LOCUS BM742038
DEFINITION K-EST0014773 S1SNU5s1 Homo sapiens cDNA clone S1SNU5s1-1-B09 5', mRNA linear EST 01-MAR-2002
ACCESSION BM742038
VERSION BM742038.1 GI:19063367
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 573)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 1 row: B column: 09
High quality sequence stop: 573.
FEATURES
Location/Qualifiers
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/clone="S1SNU5s1-1-B09"
/sex="F"
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/cell_type="Lymphoblast-like"
/lab_host="Top10F"
/clone_lib="S1SNU5s1"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7

```

promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells *E. coli* Top10F⁺ with electroporation method."

ORIGIN

Alignment Scores:
 Pred. No.: 1,34e-96 Length: 573
 Score: 927.00 Matches: 180
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 69.33% Indels: 0
 DB: 12 Gaps: 0

US-10-063-735-128 (1-260) x BM742038 (1-573)

Qy	81	PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu	100
Db	3	TTCTCAGCTATCGTCTCTCAGCACAGCGGTGTAGACATCTGCATCAACATGCTGGCTTG	62
Qy	101	AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpIysAspMetPheAsnVal	120
Db	63	GGCCGGCTTGACACCTGCTCTCAGGACAGCAGTGGTTGGAAGACATGTTCAATGTG	122
Qy	121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetIysGluArgAsn	140
Db	123	ACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTTACCATCAAGAGCGGAAT	182
Qy	141	ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu	160
Db	183	GTGGACGATGGGCACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG	242
Qy	161	SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu	180
Db	243	TCTGTGACCCACTTCTATAGTGCACCAAGTATGCCGTCACTGCCTGACAGAGGACTG	302
Qy	181	ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal	200
Db	303	AGGCAGAGCTTCGGAGAGCCACAGCCACCACTCCGAGCCACAGTGCATCTCTCAGGTGTG	362
Qy	201	ValGluThrGlnPheAlaPheIysLeuHisAspLysAspProGluIysAlaAlaThr	220
Db	363	GTGGAGACACAAATTCGCCCTTCAAACTCCACGACAGGACCCCTGAGAAGGCGAGTGCACC	422
Qy	221	TyrGluGlnMetIysCysLeuIysProGluAspValAlaGluAlaValIleTyrValLeu	240
Db	423	TATGAGCAATGAAGTGTCTCAAAACCGAGGATGTGGCCGAGGCTGTATCTACGTCTC	482
Qy	241	SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr	260
Db	483	AGCACCCCGCACATCCAGATGGAGATCCAGATGAGGCCCCACGAGGAGGTGACC	542

RESULT 23
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 LOCUS K-EST0045842 S1SNUS Homo sapiens cDNA clone S1SNUS-39-A06 5', mRNA
 DEFINITION sequence.
 ACCESSION BM764342 GI:19093957
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 602)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

TITLE
 JOURNAL
 COMMENT

Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 39 row: A column: 06
 High quality sequence stop: 602.

FEATURES
 source

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 /lab_host="Top10F"
 /clone_lib="S1SNUS"
 /note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dT-selected mRNA by
 priming with dT-tailed vector. The dT-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with *E. coli* DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells *E. coli* Top10F⁺ by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Alignment Scores:
 Pred. No.: 1,46e-96 Length: 602
 Score: 927.00 Matches: 180
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 69.33% Indels: 0
 DB: 12 Gaps: 0

US-10-063-735-128 (1-260) x BM764342 (1-602)

Qy	81	PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu	100
Db	3	TTCTCAGCTATCGTCTCTCAGCACAGCGGTGTAGACATCTGCATCAACATGCTGGCTTG	62
Qy	101	AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpIysAspMetPheAsnVal	120
Db	63	GGCCGGCTTGACACCTGCTCTCAGGACAGCAGTGGTTGGAAGACATGTTCAATGTG	122
Qy	121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetIysGluArgAsn	140
Db	123	ACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTTACCATCAAGAGCGGAAT	182
Qy	141	ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu	160
Db	183	GTGGACGATGGGCACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG	242
Qy	161	SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu	180
Db	243	TCTGTGACCCACTTCTATAGTGCACCAAGTATGCCGTCACTGCCTGACAGAGGACTG	302
Qy	181	ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal	200

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303 AGCAAGAGCTTGGGAGGCCAGACCACATCCAGCCAGTGTCTCTCCAGGTGTG 362
201 ValGluThrGlnPheAlaPheLysLeuHisAspLysProGluLysAlaAlaThr 220
363 GTGAGACACAATTCGCTTCAAACTCCAGCAAGGACCTGAGAGGAGGTGCCACC 422
221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
423 TATGAGCAATGAAGTGTCTCAACCCGAGAGTGTGCCGAGGCTGTATCTACGCTCTC 482
241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
483 AGCACCCCGCCACACATCCAGATTGGAGACATCCAGATGAGGCCACGAGGAGGTGACC 542

RESULT 24
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LOCUS
DEFINITION
K-EST0034121 S1SNUS Homo sapiens cDNA clone S1SNUS-38-A10 5', mRNA
sequence.
BM755987
VERSION
BM755987.1 GI:19085602
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 640)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 38 row: A column: 10
High quality sequence stop: 640.
Location/Qualifiers
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/lab_host="SNU-5"
/clone_lib="S1SNUS"
/note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transfection of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

FEATURES
source
1..640
/organism="Homo sapiens" linear EST 06-MAR-2002
pgpin.pk004.m18 Normalized Chicken Pituitary/Hypothalamus/Pineal
Library Gallus gallus cDNA clone pgpin.pk004.m18 5', similar to
gi|13652714 ref|XP_018530.1| hypothetical protein MGC4172 [Homo
sapiens], mRNA sequence.
BI391549
BI391549.1 GI:15084831
EST.
KEYWORDS
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 678)
Porter,T.E. and Cogburn,L.A.
ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
Library USDA/IFAFS Animal Genome Project
Unpublished (2001)
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.

ORIGIN
Alignment Scores:
source
1..678

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Pred. No.: 1.62e-96 Length: 640
Score: 927.00 Matches: 180
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.33% Indels: 0
DB: 12 Gaps: 0

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US-10-063-735-128 (1-260) x BM755987 (1-640)

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QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
Db 63 GCCCGCCTCGACACCCCTGCTCTCAGGCAGCACCCAGTGGTGTGAAGGACATGTTCAATGTG 122
QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
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QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
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QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 243 TCTGTGACCACTTCTATAGTCCCAAGTATGCCGTCACTCGCTGACAGAGGACTG 302
QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 303 AGCGAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCACCGTGCATCTCTCCAGGTGTG 362
QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr 220
Db 363 GTGGAGACACAATTCGCTTCAAACTCCAGCAAGGACCCCTGAGAGGAGCTGCCACC 422
QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 423 TATGAGCAATGAAGTGTCTCAACCCGAGGATGTGGCCGAGGCTGTATCTACGCTCTC 482
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BI391549 678 bp mRNA linear EST 06-AUG-2001
pgpin.pk004.m18 Normalized Chicken Pituitary/Hypothalamus/Pineal
Library Gallus gallus cDNA clone pgpin.pk004.m18 5', similar to
gi|13652714 ref|XP_018530.1| hypothetical protein MGC4172 [Homo
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BI391549
BI391549.1 GI:15084831
EST.
KEYWORDS
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 678)
Porter,T.E. and Cogburn,L.A.
ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
Library USDA/IFAFS Animal Genome Project
Unpublished (2001)
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES
source
1..678

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/strain="Commercial broiler chicken"
/db_xref="taxon:9031"
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/tissue_type="Pituitary Gland/Hypothalamus/Pineal Gland"
/dev_stage="Embryonic (dl2,dl4,dl9); post-hatch (w1,w3,w5,w7,w9)"
/lab_host="E. Coli EMDH10B"
/clone_lib="Normalized Chicken Pituitary/Hypothalamus/Pineal Library"
/notes="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue at different ages. Single pass sequencing from 5'-end"

ORIGIN
Alignment Scores:
Pred. No.: 1.8e-96 Length: 678
Score: 927.00 Matches: 175
Percent Similarity: 88.74% Conservative: 22
Best Local Similarity: 78.83% Mismatches: 25
Query Match: 69.33% Indels: 0
DB: 12 Gaps: 0

US-10-063-735-128 (1-260) x BI391549 (1-678)
QY 6 MetGluArgTTPArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAla 25
DB 13 ATGGACGGTGGACCGGGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 72
QY 26 AlaValAlaArgAlaLeuValGlnGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
DB 73 GCGTGGCGCGGGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 132
QY 46 GlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIle 65
DB 133 GACAAGATCGAAGATTGGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 192
QY 66 ProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPheSerAlaIleArg 85
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QY 86 SerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeuAlaArgProAspThr 105
DB 253 ACCCTTCACCGAGGAGTGTATGTGTGCATCAACACGCGAGGGTGGTGGTGGTGGTGG 312
QY 106 LeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnValAsnValLeuAlaLeu 125
DB 313 CTGCTCTCAGGGAAGACAGAGGCTGGCGACATGTAGACGTCAAGTGTGGTGGTGGTGG 372
QY 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145
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QY 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
DB 433 ATTATTAAACATTAAACAGCATGAATGGTGCAGCGTGTGTGCACAGTGGTGGTGGTGG 492
QY 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
DB 493 TACAGTCCCAACCAAGTATGACGTACCGGCGCTCTACGGANNNGGTGAGGCAAGCACTAGA 552
QY 186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGluThrGlnPhe 205
DB 553 GAAGCAAGACTCATATACGAGCTACATGTATATCTCCAGACTGGTGTAGAAACGGGATTT 612
QY 206 AlaPheLysLeuHisAspLysAspProGluLysAlaAlaThrTyrGluGlnMetLys 225
DB 613 GCTTTTAAACTTCAATGATTAATGATGACCTGNNNNNNCTGCTGCACCTATGNNNNCATTCGG 672
QY 226 CysLeu 227

Db 673 TGTCTC 678

RESULT 26
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sequence.
BU212233
ACCESSION
BU212233
VERSION
KEYWORDS
SOURCE
ORGANISM
Gallus gallus (chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
1 (bases 1 to 849)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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/lab_host="DH10B"
/clone_lib="CSEQCHN03"
/notes="Organ: whole embryo; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN
Alignment Scores:
Pred. No.: 2.25e-95 Length: 849
Score: 919.00 Matches: 174
Percent Similarity: 91.28% Conservative: 25
Best Local Similarity: 79.82% Mismatches: 19
Query Match: 68.74% Indels: 1
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x BU212233 (1-849)
QY 43 ArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyrProGly 62
DB 6 CGCAGCGTGACAAGATCGAAGATTGGCAGCTGAATGCCAGATGCCGCGTACCGCTGGG 65
QY 63 ThrIleuLeuProTyrArgCysAspLeuSerAsnGluAlaAspIleLeuSerMetPheSer 82
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Db 245 ATGGCTGTGAGATCTGCACCCGAGAGGCTATCAGTCCATGAAGAGAGAAACATCGAT 304

QY 143 AspGlyHisIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerVal 162

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QY 163 ThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGln 182

Db 365 GTGCATTTTACAGTGCACCAAGTATGCAGTCAGGCCCTCACAGAGGGGCTGAGGCAA 424

QY 183 GluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGlu 202

Db 425 GAACTCAGAGAAGCAAGACTCATATACAGGTACATGTATATCTCCAGGACTGGTAGAA 484

QY 203 ThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThrTyrGlu 222

Db 485 ACGGATTTGCTTTTAACTTCATGATGATGACCTGAGAGAGCTGCTCAACACCTATGAG 544

QY 223 GlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeuSerThr 242

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QY 243 ProAlaHisIleGlnIleCysIleGlnMetArgProThrGluGlnValThr 260

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RESULT 27
BX864140
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ACCESSION BX864140
VERSION BX864140.1 GI:39962970
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 743)
Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
Contact: Guiguen Y
INRA - SCRIBE
Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenassupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0017 row: e column: 9
Seq primer: M13R.
Location/Qualifiers
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/clones="tcba0017c.e.09"

/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="Rainbow trout multi-tissues (tcba)"
/note="Vector: pT73D-pac; Clone distribution : AGENAE
Resource centre. Francois PIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Ecude du genome (JREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN
Alignment Scores:
Pred. No.: 1..15e-94 Length: 743
Score: 912.00 Matches: 174
Percent Similarity: 86.81% Conservative: 30
Best Local Similarity: 74.04% Mismatches: 30
Query Match: 68.21% Indels: 1
DB: 13 Gaps: 0
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QY 6 MetGluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAla 25
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QY 26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
Db 101 GCGATTTCGAAGGCTCTTGTCTCAGCAGCGCATGAAGGTTGTCCGCTGTGCCAGGAACGTC 160
QY 46 GlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIle 65
Db 161 GAGAAATAGAGAAATCGCAGCAGAGTGTGAGAGCGCTGGGCACAGTGGCACCCCTTGT 220
QY 66 ProTyrArgCysAspLeuSerAsnGluAlaAspIleLeuSerMetPheSerAlaIleArg 85
Db 221 CCTTACAATGTGACCTTTCAAATGAAGAGAGAGATCCTTTCCATGTTCTTGCCATCAAG 280
QY 86 SerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeuAlaArgProAspThr 105
Db 281 ACTCTCCATCAGGAGGTGGATGTGTGCATCAACAATCTGGCTGGCCCATTCAGAGTCA 340
QY 106 LeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnValAsnValLeuAlaLeu 125
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QY 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145
Db 401 TCTATCTGCACAGAGAGGCATACCGCTCTATGAGAGAGAGAGAGAGGATGATGGACAT 460
QY 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
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QY 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
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QY 186 GluAlaGlnThrHisIleArgAlaThrCysIleSer-ProGlyValValGluThrGlnPh 205
Db 581 GAGGCTAAACCCACATTCGAGCCACGCTGATATATCTCCCTGGTATAGTGGAAACGGAAAT 640
QY 205 eAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLys 225
Db 641 TGCTTTCCGACTTCACAGCCTCCATCCAGAGAAGGCTGTGTACCTACCAACAGATGAA 700
QY 225 sCysLeuLysProGluAspValAlaGluAlaValIleTyrVal 239
Db 701 GTGTTTGGAAAGCAGTCGACATTCGAGTGTGTAACGATATGTC 743

CF595166 912 bp mRNA linear EST 08-OCT-2003
LOCUS

FEATURES
source

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DEFINITION  AGENCOURT_15714115 NIH_ZGC_8 Danio rerio cDNA clone IMAGE:7015515
5', mRNA sequence.
ACCESSION   CF595166
VERSION     CF595166.1  GI:36350329
KEYWORDS   EST.
SOURCE     Danio rerio (zebrafish)
ORGANISM   Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1 (bases 1 to 912)
            NIH-MGC http://mgc.nci.nih.gov/
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: Takuya Sakaguchi and Didier Stainier
            cDNA Library Preparation: Dr. Sumio Sugano
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L14M14730 row: k column: 01
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FEATURES             source
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     1..912
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ORIGIN
Alignment Scores:
Pred. No.:      4 78e-94      Length:      912
Percent:        908.00      Matches:    169
Conservative:   82.68%      Mismatches: 41
Best Local Similarity: 66.54% Indels:       44
Query Match:    67.91%      Gaps:       0
DB:             14
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QY      6  MetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyLeuGlyAla 25
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QY      26  AlaValAlaArgAlaLeuValGlnGlnGlyLeuValValGlyCysAlaArgThrVal 45
Db      119 GCAATCGCAAAATCTTGTGCCAGCATGGATGGAAGTGTGGATGCCAGAAACGGT 178
QY      46  GlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIle 65
Db      179 GAACAAATTAAAGAACTGGCGCTGAATGTGTGTCAGTAGCGGATACAGCGGTCTGTGTT 238
QY      66  ProTyrArgCysAspLeuSerAsnGluAlaAspIleLeuSerMetPheSerAlaIleArg 85
Db      239 CCATATAAATGTGATCTTTTCAGTAGAGGATGAGTGTGTCCATGTTCTCCTGGATCAAG 298
QY      86  SerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThr 105
Db      299 GCTCAACATAAGGTTGTGATGTGTCATTAATATGCTGTTTAGCTCTGCCAGAGCCT 358
QY      106 LeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnValLeuAlaLeu 125

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Db      359 CTGTTAGTGGCAAAACCAGCAGCTGGAGGACTATGATGGACGTCAATGTTCATGGCCCTG 418
QY      126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145
Db      419 GCAGTGTGCACACGCTGAGGCTTACAGTCCATGAAGGAAGAAAGTCAATGACCGCCAT 478
QY      146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
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QY      166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
Db      539 TACACCGCTACTAATACGAGTACCCTCCACAGAAAGTTTCAGACAGAGTTACGA 598
QY      186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGluThrGlnPhe 205
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QY      206 AlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLys 225
Db      659 GCCTACCGACTTTTAGTGATGACCAAGAAAGGCTGCTATGTATAATAGTGTGTGAG 718
QY      226 CysLeuLysProGluAspValAlaGluAlaValIleTyrValLeuSerThrProAlaHis 245
Db      719 TGCCTGCAAGCTGATGACATAACCCCAAGCAGTGTGTATGTTCTTAAGTCTCCTCTCAC 778
QY      246 IleGlnIleGlyAspIleGlnMetArgProThrGluGlnVal 259
Db      779 GTCCAAATCGGTGACCTCGAGTTAAACGCTGTGGGACCGATC 820
RESULT 29
BM848012 627 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST0127637 S13KMS5 Homo sapiens cDNA clone S13KMS5-43-A10 5',
DEFINITION mRNA sequence.
ACCESSION BM848012
VERSION BM848012.1 GI:19204411
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 627)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Soeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 43 row: A column: 10
High quality sequence stop: 627.
FEATURES             Location/Qualifiers
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     /lab_host="Top10F"
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     /note="Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly
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     phosphatase (BAP) and then decapped with tabacco acid
     pyrophosphatase (TAP). The decapped intact mRNA was
     ligated with DNA-RNA linker including EcoR I site by
     treatment of T4 RNA ligase and the first strand cDNA was

```


synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Alignment Scores:

Pred. No.: 5,52e-94 Length: 627
 Score: 905.00 Matches: 176
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 67.69% Indels: 0
 DB: 12 Gaps: 0

US-10-063-735-128 (1-260) x BM848012 (1-627)

QY 1 MetAlaArgProGlyMetClnuArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 158 GGGGGCATCG 217
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 218 TCGCGCCGACATGTGGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGCTAC 277
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 61 ProGlyThrLeuIleProThrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 278 CCCGGGATTTGATCCCTTACAGATGTGACCTATCAAAATGAAGAGGACATCCTCTCCATG 337
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 338 TTCTCAGTATCCGTTCTTCAGCAGCGGTGAGACATCTGCATCAACATGCTGGCTTG 397
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 398 GCCCGGCTGACACCTGCTCTCAGCGAGCAGCAGCAGTGTGGAGGACATGTTCAATGTG 457
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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RESULT 30

BM737591

LOCUS

DEFINITION K-EST0000094 S1SNU5 Homo sapiens cDNA clone S1SNU5-21-B02 5', mRNA

ACCESSION

BM737591

VERSION

BM737591.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 582)

Kim,N.S., Hahn,X., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

TITLE
JOURNAL
COMMENT

Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 21 row: B column: 02
 High quality sequence stop: 582.

FEATURES

source

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 /lab_host="Top10F"
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 /note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tabacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F' by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Alignment Scores:

Pred. No.: 6,33e-94 Length: 582
 Score: 904.00 Matches: 175
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 67.61% Indels: 0
 DB: 12 Gaps: 0

US-10-063-735-128 (1-260) x BM737591 (1-582)

QY 86 SerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThr 105
 Db 3 TCTCAGCAGCAGCGGTGAGACATCTGCATCAACATGCTGGCTTGGCCCGCCCTGACACC 62
 QY 106 LeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnValAsnValLeuAlaLeu 125
 Db 63 CTGCTCTCAGCAGCAGCAGTGGTGGAGGACATGTTCAATGTGAACGTGCTGGCCCTC 122
 QY 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145
 Db 123 AGCATCTGCACACGGGAAGCCTACCATGCAAGGAGCGGAATGTGGACGATGGGCAC 182
 QY 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
 Db 183 ATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTTACCCCTGTCTGTGACCACTTC 242
 QY 166 TyrSerAlaThrIlystYrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
 Db 243 TATAGTCCCAAGATATGCCGTCACTGCGCTGACAGAGGACTGTAGGCAAGAGCTTCGG 302
 QY 186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGluThrGlnPhe 205

Db 303 GAGGCCAGACCCATCCGACCGCTGTCATCTCCAGGTGGTGAGACACATTC 362
 Qy 206 AlpheLysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLys 225
 Db 363 GCCTTCAAACTCCACGACGACCTGAGAGGCGAGCTGCACCTATGAGCAATGAAG 422
 Qy 226 CysLeuLysProGluAspValAlaGluAlaValIleTyrValLeuSerThrProAlaHis 245
 Db 423 TGCTTCAAAACCGAGGATGTGGCCGAGGCTGTATCTAGCTCTCAGCACCCCGCAC 482
 Qy 246 lleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
 Db 483 ATCCAGATCGGAGACATCCAGATGAGGCCACGAGAGCTGACC 527

RESULT 31
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 DEFINITION mRNA sequence.

ACCESSION BM743569
 VERSION GI:19064898
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.

21C Frontier Korean EST Project 2001
 Unpublished (2002)

TITLE Genome Research Center
 JOURNAL Korea Research Institute of Bioscience & Biotechnology
 COMMENT 52 Roen-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 5 row: C column: 01
 High quality sequence stop: 550.

FEATURES Location/Qualifiers

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 /cell_line="SNU-5"
 /lab_host="Top10F"
 /clone_lib="S1SNU5s1"
 /note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library. After analyzing and
 sequencing about 2,000 ~ 3,000 colonies in original cDNA
 library, the abundant cDNAs were selected and amplified by
 PCR reaction using vector region primer including T7

promoter as 5' primer and N(dt)14 as 3' primer. The PCR
 products were used as template for synthesis of
 biotinylated single stranded RNA by in vitro transcription
 reaction. The synthesized RNA probes were hybridized with
 antisense single stranded cDNAs prepared from original
 library and incubated with avidin-gel. After removing
 DNA-RNA hybrids by centrifuge, the subtracted cDNA
 libraries were constructed by transformation of the
 remaining DNA into competent cells E. coli Top10F with
 electroporation method."

ALIGNMENT

Alignment Scores:
 Pred. No.: 1,67e-93 Length: 550
 Score: 900.00 Matches: 179
 Percent Similarity: 99.44% Conservative: 0
 Best Local Similarity: 99.44% Mismatches: 1
 Query Match: 67.31% Indels: 1
 DB: 12 Gaps: 0

US-10-063-735-128 (1-260) x BM743569 (1-550)

Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
 Db 3 TTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACAC-TGCATCAACAATCTGGCTTG 61

Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
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Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
 Db 122 AACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCTTACCAGTCCATGAAGGAGCGAAT 181

Qy 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
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 Db 302 AGGCAAGAGCTTCGGGAGGCCCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGTGTG 361

Qy 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr 220
 Db 362 GTGGAGACACAATTCGCTTCAAACTCCACGACAGGACCCCTGAGAGGACGCTGCCACC 421

Qy 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
 Db 422 TATGAGCAATAGATGTCTCAACCCGAGGATGTGGCCGAGGCTGTATCTACGTCTTC 481

Qy 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
 Db 482 AGCACCCCGCCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGGAGGTGACC 541

RESULT 32
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 LOCUS 603204005F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5269728 5',
 DEFINITION mRNA sequence.

ACCESSION BI464353
 VERSION BI464353.1 GI:15255009
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 757)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)

Percent Similarity: 75.63% Conservative: 42
 Best Local Similarity: 60.57% Mismatches: 42
 Query Match: 66.04% Indels: 26
 DB: 14 Gaps: 1

US-10-063-735-128 (1-260) x CF662388 (1-1143)

QY 6 MetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAla 25
 DB 53 ATGATCGCTGGAAGAGTGGTCTCTGTCTGCTGAGGCTTCAGTGGGAATCGGAGCT 112

QY 26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
 DB 113 GCAATCGCAAGTCTCTTGTCCAGCATGCGATGCAAGAGTATCGGTGCGCCAGAAATGTG 172

QY 46 GlyAsnIleGluGluAlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIle 65
 DB 173 GAGCAAAATTCAGAAATGGCAGCAGAAATGTGTAGTGGATTTCAGCGGCACTCTGTTC 232

QY 66 ProTyrArgCysAspLeuSerAsnGluAspIleLeuSerMetPheSerAlaIleArg 85
 DB 233 CGGTACAAATGTGATCTGTCTGTAGGAGCAGCATGATATCCATGTCTCTGGATCAAA 292

QY 86 SerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeuAlaArgProAspThr 105
 DB 293 GTTCAACATCAGGGCATTTGACGTGTGCATTAATATGCTGGTTGGCTCTCCAGAGCT 352

QY 106 LeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnValAsnValLeuAlaLeu 125
 DB 353 CTACTGAGTGGCAAACTAGTGTGCTGAGGACTATGATGATGTGAATGTAATGCGCTG 412

QY 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspGlyHis 145
 DB 413 TCAGTGTGACCCGCTGAGGCTTACCAGTCCATGAAAGAAAGAAATTCATGATGTCAT 472

QY 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
 DB 473 ATCAATTAATCAACAGTATTTGTGGACACCGGCTGCTCAACCATGCTGATGCACACTTC 532

QY 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
 DB 533 TACAGTGGCCAAATATGCAGTACGGCTCTCACAGAGGTTTGAGGCAAGAGTTACGA 592

QY 186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGluThrGlnPhe 205
 DB 593 GAGGCCAAACCACACATACGTGCACATGTATTCTCTCTGCTGTAGTGAGACAGAAATTT 652

QY 206 AlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLys 225
 DB 653 GCCTACCGACTCTTTAGCGAACCACCAAGATAGCTGTGCTACCTACACAAAGTGAAG 712

QY 225 ----- 225

DB 713 GTATAGACAAATTCATGATTCCTTACTATACAAAGNNTGAAGTCATCATTTATGTGTT 772

QY 226 -----CysLeuLysProGluAspValAlaGluAlaValIleTyrVal 239
 DB 773 TAAGTGTCAATTTACAGTGCCTTACAGCAGTGTGACATCCCACTCAGTGGGGTAGTTC 832

QY 240 LeuSerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGln 258
 DB 833 CTGAGTGCTCTCTCATGTTCATATTTGGTGCATTCAGATCACCACCCANNTGGAGCAG 889

RESULT 34
 B1546418
 LOCUS
 DEFINITION B1546418 714 bp mRNA linear EST 05-SEP-2001
 603198719F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5260037 5',
 mRNA sequence.

ACCESSION B1546418
 VERSION B1546418.1 GI:15433730
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 714)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M11655 row: f column: 06
 High quality sequence stop: 704.

FEATURES

Location/Qualifiers

1..714

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5260037"

/tissue type="hippocampus"

/lab host="DH10B"

/clone lib="NIH MGC 95"

/note="Organ: brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
 (gtcgag); Oligo-dT primed using primer
 5'-TTTTTTTTTTTNN-3', size-selected for average
 insert size 2.5 kb and normalized to 10^5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: this
 is a NIH_MGC Library."

ORIGIN

Alignment Scores: 3.65e-91 Length: 714
 Pred. No.: 881.50 Matches: 187
 Score: 81.39% Conservative: 1
 Percent Similarity: 80.95% Mismatches: 6
 Best Local Similarity: 65.93% Indels: 38
 Query Match: 12 Gaps: 2
 DB:

US-10-063-735-128 (1-260) x B1546418 (1-714)

QY 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
 DB 129 ATGGCCAGCCCGCATGGAGCGGTGGCGCGCGCTG----- 167

QY 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
 DB 168 -----GGGCTGCTCCAGCAGCGGACTGAAGGTGGTGGC 200

QY 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
 DB 201 TGGCCCGGCACTGTGGCGAAC----- 221

QY 61 ProGlyThrLeuIleProTyr-ArgCysAspLeuSerAsnGluGluAspIleLeuSerMe 80
 DB 222 -----ATCGAGATGTGACCTATCAATGAAGAGACATCCTCTCCAT 263

QY 80 tPheSerAlaIleArgSerGlnHisSerGlyValAspIleCys-IleAsnAsnAlaGlyL 100
 DB 264 GTTCTCAGTATCCGTTCTCAGCACACGCGGTGTAGACATCTGCAGTCAACAATGCTGGCT 323

QY 100 euAlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnV 120
 DB 324 TGGCCCGGCTGACACCTCTCTCAGGACAGCAGTGGTTGGAAGACATGTTCAATG 383

QY 120 alAsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgA 140
 Db 384 TGAACGTGCTGGCCCTCAGCATCTGCACAGGGAAGCCTACCGACCCATGAAGAGCGGA 443
 QY 140 snValAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProL 160
 Db 444 ATGTGACCATGGCCACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 503
 QY 160 euSerValThrHisPheTyrSerAlaThrIleTyrAlaValThrAlaLeuThrGluGlyL 180
 Db 504 TGCTGTGTGACCACTTCTATAGTGCACCAAGTATGCCGTCACTGGCTGCACAGGGAC 563
 QY 180 euArgGlnLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyV 200
 Db 564 TGAGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCAGTGCATCTGCCAGGTG 623
 QY 200 alValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaT 220
 Db 624 TGGTGAGACACAATTCGCTTCAAACTCCAGCACAGGACCTGAGAGGCGAGCTGC-A 682
 QY 220 hrTyrGluGlnMetLysCysLeuLysPro 229
 Db 683 CATATGACAAATGAAGTGGGGCTCC 711

RESULT 35
 AL868596 654 bp mRNA linear EST 03-DEC-2003
 LOCUS AL868596 XGC-egg Silurana tropicalis cDNA clone TBgg124024 5', mRNA
 DEFINITION
 AL868596
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Silurana tropicalis (western clawed frog)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 Xenopodinae; Silurana.
 1 (bases 1 to 654)
 Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
 Sanger Xenopus tropicalis EST project 2001 (11_2003)
 JOURNAL
 COMMENT
 On Sep 15, 2002 this sequence version replaced gi:22888861.
 Contact: Taylor R
 Sanger Institute
 Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS_SEQUENCE_ID: TEGg124024.pikSP6
 Sequencing primer: SP6
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.
 cDNA was oligo dT primed from Sug of poly A+ RNA from egg.
 EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
 5' end and NotI at the 3' end.
 Vector: pCS107; Site 1: EcoRI; Site 2: NotI
 Host: Escherichia coli XLI-blue.
 Location/Qualifiers
 1. .654
 /organism="Silurana tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:9364"
 /clone="TEGg124024"
 /dev_stage="egg"
 /lab_host="Escherichia coli XLI-blue"
 /clone_lib="XGC-egg"
 /note="vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
 was oligo dT primed from Sug of poly A+ RNA from egg.
 EcoRI-NotI cut cDNA was then ligated into pCS107 with
 EcoRI at the 5' end and NotI at the 3' end"

FEATURES

source
 CF225840 1001 bp mRNA linear EST 04-AUG-2003
 AGENCOURT_15064616 NICHDR_XGC Embs Silurana tropicalis cDNA clone
 IMAGE:6982160 5', mRNA sequence.
 CF225840
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Silurana tropicalis (western clawed frog)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 Xenopodinae; Silurana.
 1 (bases 1 to 1001)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 COMMENT
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bidg. 31 Rm10A07 Bethesda, MD 20892

ORIGIN

Alignment Scores:
 Pred. No.: 6.09e-91 Length: 654

Score: 879.00 Matches: 168
 Percent Similarity: 89.90% Conservative: 19
 Best Local Similarity: 80.77% Mismatches: 21
 Query Match: 65.74% Indels: 0
 DB: 9 Gaps: 0

US-10-063-735-128 (1-260) x AL868596 (1-654)

QY 6 MetGluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAla 25
 Db 31 ATGGAGCGCTGGAAGGCGAGCGGTGGACATTGTGACCGGGGCTCGGTGGCAATCGGAGCC 90
 QY 26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
 Db 91 GGGGTTCGCGGGTGTGTTTCAGCATGGCATGAAGTGGTGGCTGTGCCAGGAGCGTT 150
 QY 46 GlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIle 65
 Db 151 GATAAGATTGAACTGGCTGCTGAATGTCAGAGTGTGGCTACCGACGACCTTATT 210
 QY 66 ProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPheSerAlaIleArg 85
 Db 211 CCTTATAAATGTGACCTGTCCAATGAAGAGGAGATTCTGCCATGTTTCACCAATTAAG 270
 QY 86 SerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeuAlaArgProAspThr 105
 Db 271 ACTTTGTCATCAGGGGTGCGATGTATGATCAACAATGCAGGCTTGGCCGCGAGCGCT 330
 QY 106 LeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnValAsnValLeuAlaLeu 125
 Db 331 TTGCTGAGTGGCAAAACAGAGGAGTGGAGACAATGATTGATGTTTAAATGTTTTCGACTC 390
 QY 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145
 Db 391 AGTATCTGCACAGAGAGCGCTACCACTCCATGAAGAAAGAAATATCATGATGGCCAT 450
 QY 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
 Db 451 ATCATAAATCAATCAACAGCATGAGTGGCCATAGATTCTTCTTCTACAGTTATGCACATT 510
 QY 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnLeuArg 185
 Db 511 TATTGAGTACTAAGTATGCTGTAACTGCCCTGACAGAGGCGCTCAGGCAAGAGCTCAGA 570
 QY 186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGluThrGlnPhe 205
 Db 571 GAAGAAAAGAGTCAATCCGAGCAACGAGTATATCGCCAGCGCTTGGAAACCTGGATT 630
 QY 206 AlaPheLysLeuHisAspLysAsp 213
 Db 631 GCATTAAACTCTCTTGATAATGAT 654

RESULT 36

CF225840

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Email: cgaabs-remail.nih.gov
 Tissue Procurement: Robert M. Grainger
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LLAM14644 row: 1 column: 07
 High quality sequence stop: 674.

FEATURES

Location/Qualifiers

1..1001
 /organism="Silurana tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="IMAGE:6982160"
 /tissue_type="tadpole"
 /dev_stage="embryo, stages 40-45"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NICHD XGC Emb8"
 /note="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV;
 Cloned unidirectionally. Primer: Oligo dt. Average insert
 size 2.1 kb. Constructed by Invitrogen. Note: This is a
 Xenopus Gene Collection (XGC) library."

ORIGIN

Alignment Scores:
 Pred. No.: 1,08e-89 Length: 1001
 Score: 871.00 Matches: 162
 Percent Similarity: 81.86% Conservative: 32
 Best Local Similarity: 68.35% Mismatches: 43
 Query Match: 65.15% Indels: 0
 DB: 14 Gaps: 0

US-10-063-735-128 (1-260) x CF25840 (1-1001)

QY 22 GlylleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCys 41
 DB 5 GGCATCGGAGCGCGGTTGCCCGGGTGTTCAGCATGGCATGAAGTGTGGCGTGT 64
 QY 42 AlaAgtThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyrPro 61
 DB 65 GCACAGAGCGTTGATAAGATTGAGAACTGGCTGCTGATGTCAGAGTCTGGCTACCA 124
 QY 62 GlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPhe 81
 DB 125 GGCACCTTATTCCTTATAATGTGACCTGTCCATGAAGAGGAGATTCCTCCATGTTT 184
 QY 82 SerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeuAla 101
 DB 185 TCAGCAATAAAGACTTTGCATCAGGGGGTGCATGTAATGATCAACATGACGCTTGGCC 244
 QY 102 ArgProAspThrLeuLeuSerGlySerThrSerGlyTyrPlyAspMetPheAsnValAsn 121
 DB 245 CGACCGGAGCCITTCCTGAGTGCACAACAGAGGGATGAGAACATGATGATTAAT 304
 QY 122 ValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnVal 141
 DB 305 GTTCTTGCACTCAGTATCTGCACAAGAGAGGCGCTACAGTCCATGAAGAAAGATAATC 364
 QY 142 AspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSer 161
 DB 365 GATGATGGCCATATCATTAACATCAACAGTGTCTTGGCCATATCTACCAATGTGCAAA 424
 QY 162 ValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArg 181
 DB 425 CAGGCTCCTTTTATTGTGTCACCAAGCATACAGTCAGCGCGCTCCTGAAGCGATAAGA 484
 QY 182 GlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValVal 201
 DB 485 CRAAGAGCTGAGAAATTTGAAGAGCCATATTCGTGTTACAGACATTTCCCTGGCCCTGTG 544
 QY 202 GluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThrTyr 221

Db 545 GAGACAAATTTGCTTACAGATGTTTGAATAACCCGTCATAGCAGCTACGCTGTAC 604
 QY 222 GluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeuSer 241
 Db 605 AAATCAATTAAGTGTCTTGTATCTCGTGATATCTGTAATCTGTTTATATGCTCTGGGT 664
 QY 242 ThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGln 258
 Db 665 ACACCACCTCATGTTTCAGGTTTCATGAATGATTGTGAGACCACTGACCA 715

RESULT 37

BI765897

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 804)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM14645 row: 1 column: 12

High quality sequence stop: 748.

Location/Qualifiers

1..804

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5186459"

/lab_host="DH10B"

/clone_lib="NIH_MGC_116"

/note="Organ: pooled colon, kidney, stomach; Vector:

pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA

source anonymous pool of 3 colons, age 26 yo male, 49 yo

female, 71 yo male colon, 46 yo male kidney, and pool of 2

stomachs, 62 yo male and 70 yo female. Library is

oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.4 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

023. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 2.15e-89 Length: 804

Score: 867.00 Matches: 193

Percent Similarity: 93.33% Conservative: 3

Best Local Similarity: 91.90% Mismatches: 4

Query Match: 64.85% Indels: 10

DB: 12 Gaps: 0

US-10-063-735-128 (1-260) x BI765897 (1-804)

QY 1 MetAlaArgProGlyMetGluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSer 20

Db 194 ATGCCAGGCGCCGGCATGAGCGGTGCGCGACCGCGCTGGCGTGTGTGACGGGGCGCTCG 253

```

QY 21 GlyGlyIleGlyAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 254 GGGGGCATCGCGCGCGCGTGGCGCGCGTGGTCCAGCAGGACTGAAGGTGGTGGC 313
QY 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 314 TGGCCCGGCACATGTGGGCAACATCGAGGAGCTGGCTGCTGAATGTAAAGTGCAGGCTAC 373
QY 61 ProGlyThrLeuLeuProTyrArgCysAspLeuSerAsnGluAlaAspIleLeuSerMet 80
Db 374 CCGGGACCTTGCATCCCTACAGATGACCTATCAATGAAGAGACATCCTCCCATG 433
QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100
Db 434 TTCTCAGCTATCGTTCTCAGCACGCGGTGTAGACATCTGCATCAACATGCTGGCTG 493
QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrPlyAspMetPheAsnVal 120
Db 494 GACCGGCTTGACACCTGCTCTCAGGACACACAGTGTGGAGGACATGTTCAATGTG 553
QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 554 AACGTGCTGGCCTCAGCATCTGCACAGGAGGCTACCATGCCATGAAGGAGCGAAT 613
QY 141 Val--AspAspGlyHisIleLeuAsnIleAsnSerMetSerGlyHisArgValLeuProL 160
Db 614 GTGGAGCAGTGGGACATCATTAACATCAATAGCATGTCTGCCACCGAGTGTACCCC 673
QY 160 eu-SerValThrHisPheTyr-SerAla-ThrLysTyrAla-ValThr-AlaLeuThr-G 178
Db 674 TGGTCTGTGACCCATCTTAAGTGCACCAACAGTATGCCGCTCACTGGCGCTGACAA 733
QY 178 LuGlyLeuArgGlnGlu-LeuArgGlu-AlaGlnThrHisIleArgAlaThrCysIleSe 197
Db 734 AGGACTGAGCAGAGACTTCGGAGAGCCCAACCAACCATCGAGACAAAGTGCATCTC 793
QY 197 rProGlyVal 200
Db 794 TCCAGGTGTT 803

RESULT 38
LOCUS BX773551/c
DEFINITION BX773551 XGC-egg Silurana tropicalis cDNA clone Tegg038a23 3', mRNA
sequence.
ACCESSION BX773551
VERSION BX773551.1 GI:39680756
KEYWORDS EST.
SOURCE Silurana tropicalis (western clawed frog)
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 935)
Croning,W.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
Contact: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropesanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: Tegg038a23.q1k77
Sequencing primer: T7
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dT primed from Sug of poly A+ RNA from egg.
ECORI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NotI
Host: Escherichia coli XL1-blue.
Location/Qualifiers
1..935
FEATURES
source

```

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/organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TEgg038a23"
/dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-egg"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from egg.
ECORI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"

ORIGIN
Alignment Scores: 1.99e-87 Length: 935
Pred. No.: 851.00 Matches: 158
Score: 851.00 Conservative: 32
Percent Similarity: 81.55%
Best Local Similarity: 67.81%
Query Match: 63.65%
Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x BX773551 (1-935)

QY 26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
Db 933 GCGGTTGCCCGGCTGTTGTTTCAGCATGCGATGAAGTGGTGGCTGTGCCAGGAGCGTT 874
QY 46 GlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIle 65
Db 873 GATAAGATTGGAACAACTGGCTGCTGAATGTCAGATGCTGCTACCCAGGACCTTATT 814
QY 66 ProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPheSerAlaIleArg 85
Db 813 CCTTATAATGTGACCTGTCCATGAAGAGGAGATTCGTCCATGTTTTCAGATAAAG 754
QY 86 SerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeuAlaArgProAspThr 105
Db 753 ACTTGTGATCAGGGGGTGCATGTATGATATCAACATGCAGGCTTGGCCCGAGCGCT 694
QY 106 LeuLeuSerGlySerThrSerGlyTyrPlyAspMetPheAsnValAsnValLeuAlaLeu 125
Db 693 TTGCTGAGTGGCAAAACAGAGGATGAGAAACAATGATGATGATGATGATGATGATGAT 634
QY 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspGlyHis 145
Db 633 AGTATCTGCACAGAGAGGCTTACCACTCCATGAAGGAAGGATATCGATGATGCGCAT 574
QY 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
Db 573 ATCAATAACATCAACAGTGTCTTGGCCATATCTACCAATGTGCAAAACAGGCTCACTTT 514
QY 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
Db 513 TATTGTGCCACCAAGCATACAGTGACGGCGCTCCTGAGACCGATAGACAGAGCTGAGA 454
QY 186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGluThrGlnPhe 205
Db 453 GAATTGAAGAGCCATATTCGTGTACAGCATTTCCCTCGCCTTGTGGAGACAGAAATTT 394
QY 206 AlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLys 225
Db 393 GCTTACAGATGTTTTGAAAATGACCCGCTCAATAGCAGCTACGCTGTACAATCAATTAAG 334
QY 226 CysLeuLysProGluAspValAlaGluAlaValIleTyrValLeuSerThrProAlaHis 245
Db 333 TGCTTTGATCCTGGTGTATCGCTAATGCTGTTTATATGCTCTGGGTACACACCTCAT 274
QY 246 IleGlnIleGlyAspIleGlnMetArgProThrGluGln 258
Db 273 GTTCAGGTTTCATGAATGATTGTGAGACCACTGACCAA 235

RESULT 39
BF581815

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LOCUS      BF581815                946 bp    mRNA    linear    EST 12-DEC-2000
DEFINITION 602099816F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4219994 5',
            mRNA sequence.
ACCESSION  BF581815
VERSION     BF581815.1 GI:11655527
KEYWORDS    Mus musculus (house mouse)
SOURCE      Mus musculus
ORGANISM    Mus musculus
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LAM9802 row: 0 column: 03
            High quality sequence stop: 646.
            Location/Qualifiers
              1..946
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="FVB/N"
                /db_xref="taxon:10090"
                /clone="IMAGE:4219994"
                /lab_host="DH10B (T1 phage-resistant)"
                /clone_lib="NCI CGAP Co24"
                /note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 1.6 kb. Constructed by Life
            Technologies. Note: this is a NCI_CGAP Library."
FEATURES             source
source
ORIGIN
Alignment Scores:
Pred. No.:          7 71e-87          Length:          946
Score:              846.00            Matches:         201
Percent Similarity: 81.37%            Conservative:    13
Best local Similarity: 76.43%          Mismatches:      39
Query Match:        63.28%            Indels:          13
DB:                  10                Gaps:            3

US-10-063-735-128 (1-260) x BF581815 (1-946)

QY      1  MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db      66  ATGACTAGAGCTGGCATGGAGCGGTGGCGCGACCGGCTGGCACTGGTGCAGCGGAGCTCG 125
QY      21  GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db      126  GGGGGCATCGGTGGCGCCGTGGCCCGGGCATTAGTCCAGAGGAGTGAAGGTGTGGGT 185
QY      41  CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db      186  TGTGCCCGCACCGTGTGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGATGTCAGGCTAC 245
QY      61  ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluAluAspIleLeuSerMet 80
Db      246  CCGGGACTTTGATCCCTTACAGATGTGACCTGTCAATGAGGAGACATCTCTCTCCATG 305
QY      81  PheSerAla-IleArgSerGlnHisSerGlyValAlaAspIleCysIleAsnAlaGlyLe 100
Db      306  TTTCTAGCATGTCGATCCGACACAGTGGCGGTGGATCTATCTGATCAACATGCCGGCAT 365
QY      100  uAlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVa 120
Db      366  GGCCG--GCTGACACCTGTCTCTCGGGCAGCACCAGCGGATGGAAGACATGTTCAATGT 423

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QY      120  lAsnValLeuAlaLeuSerIleCysThrArg-GluAlaTyrGlnSerMetLysGluArg 140
Db      424  GAATGTGCTGGCCCTCAGCATCTGCACCTCTGGGAGGCTTATCAGTCCATGAGGAGCGGA 483
QY      140  snValAspAspGlyHisIleIleAsn-IleAsnSerMetSerGlyHisArgValLeuPro 159
Db      484  ACATAGACGACGGGCACATCATTAACAATCAACAGCATGTGTGGCCACCGAGTCCACCC 543
QY      160  LeuSerValThrHisPhe-TyrSerAlaThrLysTyrAlaValThrAlaLeuThr-GluG 179
Db      544  CAGTCTGTGATCCATTTCTAATAGTGGACTAAGTATGCCGTCCACTGACACTGACAAGAGG 603
QY      179  lLeuArgGlnGluLeu-ArgGluAlaGlnThrHisIleArgAlaThrCysIleSerPro 198
Db      604  GACTCAGGCAAGACTTCTTGGAGGCCAGAGCCATATCCGGCAACGATGATTCTTCAG 663
QY      199  GlyValValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAla 218
Db      664  GCTTGGTTAGACACACAGCTTCGCTTCCAACTCATGAACAGACGGGGAA---GCAGGT 720
QY      219  AlaThrTyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyr 238
Db      721  GCCCC-TATGAACACGTA---TGTGTTTCAGACAGAGACGTGCTTGGGCTGTCTATATAG 776
QY      239  ValLeuSerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGlu 257
Db      777  TTACTAGGAGACCCCA-----CAGTCGGTGGACACTCAGTCGCCCGCAGCAG 826

RESULT 40
LOCUS    BI761329                748 bp    mRNA    linear    EST 25-SEP-2001
DEFINITION 603044093F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5184479 5',
            mRNA sequence.
ACCESSION  BI761329
VERSION     BI761329.1 GI:15752907
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 748)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LAM11460 row: i column: 24
            High quality sequence stop: 724.
            Location/Qualifiers
              1..748
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:5184479"
                /lab_host="DH10B"
                /clone_lib="NIH MGC 116"
                /note="Organ: pooled colon, kidney, stomach; Vector:
            pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
            source anonymous pool of 3 colons, age 26 yo male, 49 yo
            female, 71 yo male colon; 46 yo male kidney, and pool of 2
            stomachs, 62 yo male and 70 yo female. Library is
            oligo-dT primed and directionally cloned (EcoRV site is
            destroyed upon cloning). Average insert size 1.4 kb,
            insert size range 1-3 kb. Library is normalized and
            enriched for full-length clones and was constructed by C.

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Contact: Andrew R. Cossins

8	ArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyLeuGlyAlaVal	27
42	CGCTGGAAAGGTAGGGTGTCTTGTCTACTGGAGCTTCAGTGGGAATCGGAGCTGCAATC	101
28	AlaArgAlaLeuValGlnGlnGlyLeuIysValValGlyCysAlaArgThrValGlyAsn	47
102	GCAAAGTCTCTTGTCCAGCATGCGATCAGAGGTATCGGTGCGCCAGAAATGTGGAGCAA	161
48	IleGluIuLeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIleProTyr	67
162	ATTCAAGAACTGCGCAGCAGAATGTGTAGTAGTGATTCGGCGCACTCTGTTCGGTAC	221
68	ArgCysAsnLeuSerAsnGluAlaAspIleLeuSerMetPheSerAlaIleArgSerGln	87
222	AAATGTATCTGTCTGTAGAGCAGCATGATCATCATCTTCCTGGATCAAGTTCOA	281
88	HisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThrLeuLeu	107
282	CATCAGGCGATTGACGTGTGCATTAAATGCTGGTTTGGCTCTCCAGAGCCTCTACTG	341
108	SerGlySerThrSerGlyTrpLysAsp	116
342	AGTGGCAAACTAGTGGCTGGAG-GACTATGATGGATGTATGTAACCTCAAAATAAGCATT	400
117	-----MetPheAsnVal	120
401	TTCTCTATTCTAACTGCATAGTCATGCTAGTCATGCCCAAAATGTTTCATCTTTGCGAGTG	460
121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn	140
461	AATGTAATTGCCCTGTCACTGTGCACCCGTGAGGCTTACCACTCCATGAAGAAGAAAA	520
141	ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu	160

521 ATTGATGATGCTATATCATATATATCAACAGTATTTGTGGACACCGGTCGTCAACCAT 580
Db
161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Qy
581 GCTGATGCACACTTCTACAGTGCAGCAATATATGACGTGACGGCTCTCACAGAAGTTTG 640
Db
181 ArgGlnGluLeuArgGluAlaGlnThrHisIleAlaThrCysIleSerProGlyVal 200
Qy
641 AGCAAGAGTTACGAGAGGCCAAACCCACATACGTGCCACATGATTAATTTCTCTGGCTTA 700
Db
201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr 220
Qy
701 GTGAGAGCAGAAATTGGCTACCGACTCTTTAGCGAANACCAGGAATAGCTGTGCTACC 760
Db
221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Qy
761 TACCAAGTGTAAAGTGCCTACAGCCATTGACCTCGCCAACTCAGTGGTGTATGCTCG 820
Db
241 SerThrProAlaHisIleGlnIleGlyAspIleGln 252
Qy
821 AAGCTCCCTCCCTGTTCCCAATTGGGACATTGAGA 856
Db
RESULT 42
AL845993 646 bp mRNA linear EST 20-NOV-2003
LOCUS
DEFINITION AL845993 XGC-egg Silurana tropicalis cDNA clone TEgg062g24 5', mRNA
sequence.
ACCESSION AL845993
VERSION AL845993.2 GI:38487078
KEYWORDS
SOURCE
ORGANISM
EST.
Silurana tropicalis (western clawed frog)
Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae;
Xenopodinae; Silurana.
1 (bases 1 to 646)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
On Sep 15, 2002 this sequence version replaced gi:22866258.
Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TEgg062g24.p1kSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn. 5ug of poly A+ RNA from egg.
cDNA was oligo dt primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XL1-blue.
Location/Qualifiers
FEATURES
source
1..646
/organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TEgg062g24"
/dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-egg"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"

521 ATTGATGATGCTATATCATATATCAACAGTATTTGTGGACACCGGTCGTCAACCAT 580
Query Match: 81.44% Mismatches: 18
DB: 62.23% Indels: 0
Gaps: 0
US-10-063-735-128 (1-260) x AL845993 (1-646)
Qy 6 MetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAla 25
Db 63 ATGAGGCGCTGGAAAGCGGCGGCTGTTGTGACCGGCGCTGGTGGGCGATCGGAGCC 122
Qy 26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
Db 123 GCGGTTGCGGCGGCTGTTGTCAGCATGGCATGAAGTGGTGGCTGTGCGCAGGCGTT 182
Qy 46 GlyAsnIleGluGluLeuAlaGluCysSerAlaGlyTyrProGlyThrLeuIle 65
Db 183 GATAAAGATTGAGAACTGGCTGCTGAATGTCAAGTGTGCTGCTGCTGCTGCTGCTTATT 242
Qy 66 ProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPheSerAlaIleArg 85
Db 243 CCTTATAAATGTGACCTGTCCAATGAAGAGAGGATCTGTCCATGTTTTCAGCAATAAG 302
Qy 86 SerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeuAlaArgProAspThr 105
Db 303 ACTTTGCATCAGGGGCTGATGTATGATCAACAATGCAGGCTTGGCCGACCGAGCCT 362
Qy 106 LeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnValAsnValLeuAlaLeu 125
Db 363 TTGCTGATGGCAAAACAGAGGGATGGAGAACAAATGATGATGTTAAATGTTTCTTGCATC 422
Qy 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145
Db 423 AGTATCTGCACAGAGAGCCCTACAGTCCATGAAGAAAGAAATATCGATGATGCCAT 482
Qy 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
Db 483 ATCATAAACATCAACAGCATGAGTGGCCATAGAGTTCTTCTCTACAGTTATGCACTTT 542
Qy 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
Db 543 TATTGAGTACTAAGTATGCTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 602
Qy 186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGly 199
Db 603 GAAGAAAGAGTGCATCCGAGCAACGAGTATATCGCCAGGC 644
RESULT 43
CD469548 672 bp mRNA linear EST 04-JUN-2003
LOCUS
DEFINITION LeukoS2_4_F10_g1_A024 Stimulated peripheral blood leukocytes S2
Equus caballus cDNA clone LeukoS2_4_F10_A024 5', mRNA sequence.
ACCESSION CD469548
VERSION CD469548.1 GI:31390816
KEYWORDS
SOURCE
ORGANISM
Equus caballus (horse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
1 (bases 1 to 672)
Vandenplas,M., Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S.,
Moore,J.N., Liang,C., Sun,F., Sullivan,R., Shah,M. and Pratt,L.H.
An EST database from equine (Equus caballus) stimulated peripheral
blood leukocytes
Unpublished (2003)
Other ESTs: LeukoS2_4_F10_b1_A024
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in

the Human Genome Center, University of Tokyo Institute of Medical Science; tissue and RNA were prepared in the Department of Large Animal Medicine, University of Georgia; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Seq primer: Sug5 (CTTCTGCTCAAAAGCTGG).

FEATURES

Location/Qualifiers
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/organism="Equus caballus"
/mol_type="mRNA"
/strain="thoroughbred"
/db_xref="taxon:9796"
/clone="LeukoS2_4_F10_A024"
/sex="male"
/tissue_type="blood"
/cell_type="leukocytes"
/lab_host="DH10B-TI phage-resistant E. coli"
/note="Organ: circulatory system; Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from equine peripheral blood leukocytes isolated from a healthy adult horse. The leukocytes were stimulated for 4 hr with 10 ng/ml E. coli O55:B5 LPS. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5'-prime DraIII site is CACTGTGTG, 3'-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Alignment Scores:
Pred. No.: 1.49e-84 Length: 672
Score: 824.00 Matches: 170
Percent Similarity: 69.72% Conservative: 5
Best Local Similarity: 67.73% Mismatches: 6
Query Match: 61.63% Indels: 70
DB: 14 Gaps: 1

US-10-063-735-128 (1-260) x CD469548 (1-672)

QY 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 130 ATGCCAGGCGCGGATGAGCGGTGGCTGACCGCTGGCTGTTAACCAGGACCTCG 189
QY 21 GlyGlyLeuGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuValValGly 40
Db 190 GGGGGCATGGCGCGCGTGGCGCGGCGCTGGTCCAGCGGACCTTAAGGTGGTGGGT 249
QY 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 250 TGCCTCCGCGACCGTGGGCAACATCGAG-----276
QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
Db 276 -----276
QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
Db 276 -----276
QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
Db 277 -----GTG 279
QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 280 AACGTGTCGCCCTCAGCATCTGCACACGGGAGCCTACCAGTCCATGAAGGCGGAAA 339
QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 340 GTGATGACGGGCACATCATTAACATCAACAGCATGTCTGCCACCAGGTGGTACCCCG 399

QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 400 TCATGACCACTTCTATAGTCCCAAGATATGCCGTCACTCACTGACAGAGGACTG 459
QY 181 AtgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 460 AGCAAGAGCTTCGGAGGAGCCAGACCCACATCCGAGCCACGTGCAATTTCTCCAGGATTG 519
QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGlyLysAlaAlaThr 220
Db 520 GTGGAGACACAGTTCGCTTCAACTCCACGACAGGACCTTGAGAAACAGCTGCCACC 579
QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 580 TATGAGCATAAAGTGTCTCAAGCTGAGGATGTGGCGGAGCTGTCATCTATGTCTTC 639
QY 241 SerThrProAlaHisIleGlnIleGlyAspIle 251
Db 640 AGCAGCGCCCCCAATGTCAGATTGGAGACATC 672
BE869917 614 bp mRNA linear EST 20-OCT-2000
601446563F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850574 5',
mRNA sequence.
BE869917
BE869917.1 GI:10318693
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 614)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9569 row: n column: 15
High quality sequence stop: 602.
Location/Qualifiers
1..614
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3850574"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_65"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."

FEATURES

source
1..614
Alignment Scores:
Pred. No.: 5.33e-83 Length: 614
Score: 810.00 Matches: 175
Percent Similarity: 97.77% Conservative: 0
Best Local Similarity: 97.77% Mismatches: 4
Query Match: 60.58% Indels: 4
DB: 10 Gaps: 0
US-10-063-735-128 (1-260) x BE869917 (1-614)

ORIGIN

QY 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20

Oligo dT. Average insert size 1.95 kb. Constructed by Resgen, Invitrogen Corp. Note: this is a NIH_MGC Library."

Oligo dT. Average insert size 1.95 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library.	
ORIGIN	
Alignment Scores:	2.34e-82 Length: 977
Pred. No.:	807.50 Matches: 164
Score:	85.64% Conservative: 3
Percent Similarity:	84.10% Mismatches: 8
Best Local Similarity:	60.40% Indels: 20
Query Match:	13 Gaps: 1
DB:	
US-10-063-735-128 (1-260) x BU839980 (1-977)	
Qy	1 MetAlaArgProGlyMetGluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db	104 ATGACTAGAGTGGCAGCGGTGGCGCCGCGCTGGTGGCCTGGTGGACGGGAGCTCG 163
Qy	21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db	164 GGGGCGCATCGTGGCGCGCTGGCCGGGCATTAGTCCAGCAGGAGACTGAAGTGTGGGT 223
Qy	41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db	224 TGTGCCGCGCACCGTTGGCAAC----- 244
Qy	61 ProGlyThrLeuIleProTyr-ArgCysAspLeuSerAsnGluAlaAspIleLeuSerMe 80
Db	245 -----ATCGAGATGTGACCTGTCAATGAGGAGGACATCTCTCCAT 286
Qy	80 tPheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLe 100
Db	287 GTTCTCAGCTGTCGATCCAGCACAGTGGCGTGGATATCTGCATCAACAATGCCGCAT 346
Qy	100 uAlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVa 120
Db	347 GGCCCGGCGCTGCACACCTGCTCTCGGGCAGCACCGCGGATGGAAGGACATGTTCAATGT 406
Qy	120 IasnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAs 140
Db	407 GAATGTGTGGCCCTCAGCATCTGCATCGGGAGGCTTATCACTCATGAAGAGCGGAA 466
Qy	140 nValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLe 160
Db	467 CATAGCAGCGGGCACATCATTAACATCAACAGCATGTGTGGCCACCGAGTCCACCCCA 526
Qy	160 uSerValThrHisPheTyrSerAlaThrIleTyrAlaValThrAlaLeuThrGluGlyLe 180
Db	527 GTCTGTGATCCATTTCTATAGTGGCAGTAAAGTATGCCGTCATGCACTGACAGGGACT 586
Qy	180 uArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThr 194
Db	587 CAGGCAAGAGCTTCTGGAGGCCAGACCCATATCCGGGCCACG 629
RESULT 46	
LOCUS	W58472 567 bp mRNA linear EST 15-OCT-1996
DEFINITION	z25b06.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone
IMAGE:341651 5' similar to SW:Y0XD_BACSU P14802 HYPOTHETICAL 25.3	
KD PROTEIN IN RTP 5'REGION ; mRNA sequence.	
ACCESSION	W58472
VERSION	W58472.1 GI:1365185
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 567)
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Matra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasaki,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE JOURNAL COMMENT

The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1354 Std Error: 0.00
Seq primer: mob. REGA-RT
High quality sequence stop: 351.

FEATURES

source
1..567
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1267026"
/db_xref="taxon:9606"
/clone="IMAGE:341651"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart_NBH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACCAATCTGAATGGAGCGCGGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBH19W."

ORIGIN

Alignment Scores:
Pred. No.: 5,11e-82 Length: 567
Score: 801.00 Matches: 175
Percent Similarity: 93.58% Conservative: 0
Best Local Similarity: 93.58% Mismatches: 4
Query Match: 59.91% Indels: 8
DB: 14 Gaps: 0
US-10-063-735-128 (1-260) x W58472 (1-567)
QY 50 GluLeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIleProTyrArgCys 69
Db 18 GAGCTGGCTGCTGAATGTAAAGTGTGAGGTACCCCGGAGCTTTGATCCCTACAGATGT 77
QY 70 AspLeuSerAsnGluGluAspIleLeuSerMetPheSerAlaIleArgSerGlnHisSer 89
Db 78 GACCTATCAATAGAGGAGCATCTCTCATGTCTCAGTATPCCGTCTCAGCAGC 137
QY 90 GlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThrLeuLeuSerGly 109
Db 138 GCTGTAGACATCTGCATCAACATGCTGGCTTGGCCGGCTGACACCTCTCTCAGGC 197
QY 110 SerThrSerGlyTyrIlyAspMetPheAsnValAsnValLeuAlaLeuSerIleCysThr 129
Db 198 AGCACCAGTGGTGGAGGAGCATGTTCAATGTGAACGTGTGGCCCTCAGCATCTGCACA 257
QY 130 ArgGluAlaTyrGln-SerMetLysGlu-ArgAsnValAsp-AspGlyHisIleAs 148
Db 258 CGGGAAGCTACCAAGTCCATGAGGAGCGGAATGTGGACCNATGGGCATCAATTA 317
QY 148 nIleAsn-SerMetSerGlyHis-ArgValLeuProLeuSerValThrHisPheTyrSer 167
Db 318 CATCAATAAGCATGTCTGGCCACCCGAGTGTACCCCTGTCTGTGACCCACTTCTATAGT 377
QY 168 AlaThrLysTyrAlaValThrAlaLeuThrGluLeuArgGlnGluLeuArgGluAla 187

Db 378 GCCACCAAGTATCCCTCACTGCGCTGACAGAGGAGCTGAGGCAAGAGCTTCGGAGGCC 437
QY 188 GlnThrHisIleArgAlaThrCysIleSerProGlyVal-ValGluThrGlnPheAlaPh 207
Db 438 CAGACCCACATCCGAGCCAGCTGCACTCTCCAGGTGTGGTGGAGACACAATTCGCTT 497
QY 207 eLysLeu-HisAspLysAspProGlyLysAlaAlaAlaThrTyrGluGlnMetLysCysL 227
Db 498 CAAACTTCCAGCACAAAGGACCCCTGAGGAAGCAGCTGCACCTATGAGCNAATGAAGTGC 557
QY 227 eLys 228
Db 558 TCAA 562
CF348186 763 bp mRNA linear EST 18-AUG-2003
AGENCOURT_15225322 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7001094
5', mRNA sequence.
CF348186
CF348186.1 GI:33791814
EST.
SOURCE
Danio rerio (zebrafish)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 763)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
COMMENT
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgepbs-remail.nih.gov
Tissue Procurement: Len Zon, Harvard
cDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMA4693 row: n column: 05
High quality sequence stop: 510.

FEATURES

source
1..763
Location/Qualifiers
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:7001094"
/tissue_type="whole body"
/lab_host="DH10B"
/clone_lib="NIH_ZGC_10"
/notes="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
Bulk tissue was collected from a whole adult individual
from the Tuebingen strain. 1st strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments. A
normalized version of this library is also available
(NIH_ZGC_7). Library was constructed by Open Biosystems
(Huntsville, AL)."

ORIGIN

Alignment Scores:
Pred. No.: 2.85e-81 Length: 763
Score: 796.50 Matches: 158
Percent Similarity: 84.96% Conservative: 34
Best Local Similarity: 69.91% Mismatches: 33
Query Match: 59.57% Indels: 3
DB: 14 Gaps: 0

RESULT 48	AL8981132	648 bp	linear	EST 04-DEC-2003
LOCUS	AL8981132			
DEFINITION	XGC-egg <i>Silurana tropicalis</i> cDNA clone TEGG038a23 5', mRNA sequence.			
ACCESSION	AL8981132			
VERSION	AL8981132.2	GI:38697669		
KEYWORDS	EST.			
SOURCE	<i>Silurana tropicalis</i> (western clawed frog)			
ORGANISM	<i>Silurana tropicalis</i>			
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; <i>Silurana</i> .			
REFERENCE	1 (bases 1 to 648)			
AUTHORS	Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.			
TITLE	Sanger Xenopus tropicalis EST project 2001 (11_2003)			
JOURNAL	Unpublished (2003).			
COMMENT	On Sep 16, 2002 this sequence version replaced gi:22950524.			
	Contact: Taylor R			
	Sanger Institute			
	Hinxton, Cambridgeshire, CB10 1SA, UK			
	Email: trop@sanger.ac.uk			

GluAlaClnThrHisLeuArgAlaThrCysIleSerProGlyValValGlnIleGlnPhe

Db 581 GAATTGAGGCCATATTCGTGTTTACAAGCAATTCCTCGCTTGTGGAGACAGAAATTT 640

QY 206 AlaPhe 207

Db 641 GCTTAC 646

RESULT 49

CD599740

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CD599740 650 bp mRNA linear EST 16-JUN-2003

RK119A4F07.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA

clone RK119A4F07 5', mRNA sequence.

CD599740

CD599740.1 GI:31780616

EST.

Danio rerio (zebrafish)

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 650)

Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W., Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T., Zou, L.I. and Chen, Z.

Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue

Unpublished (2003)

Contact: Chen Z.

State Key Lab for Medical Genomics

Shanghai Institute of Hematology, Ruijin Hospital Affiliated to Shanghai Second Medical University

197 Rui Jin Road II, Shanghai 200025, P. R. China

Tel: 86-21-64740490

Fax: 86-21-64743206

Email: zchen@sh.sh.cn

Seq primer: T3.

FEATURES

source

1. 650

Location/Qualifiers

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="RK119A4F07"

/dev_stage="mature"

/clone_lib="Zebrafish Kidney Marrow cDNA library"

/note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI; Site 2: EcoRI; Total RNA was extracted from the kidney tissues of mature zebrafish. The poly (A)+ RNA fraction was separated from total RNA by oligo (dT) cellulose chromatography. Library was initially constructed in the lambdaZAP Express vector (Stratagene) and in vivo excised into pBS-CMV vector."

ORIGIN

Alignment Scores:

Pred. No.: 3.54e-80 Length: 650

Score: 786.00 Matches: 147

Percent Similarity: 87.37% Conservative: 26

Best Local Similarity: 74.24% Mismatches: 25

Query Match: 58.79% Indels: 0

DB: 14 Gaps: 0

US-10-063-735-128 (1-260) x CD599740 (1-650)

QY 6 MetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyVala 25

Db 56 ATGGATCGTGGAAAGCAGAGTGTCTTGTCTCACTGGAGCTTCAGTAGAATAGAGCT 115

QY 26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45

Db 116 GCAATCGAAAGCTCTTGTCCAGCATGGCATGAGGTGTGTGGATGCCAGAAATGTG 175

QY 46 GlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIle 65

Db 176 GAGCAATAGAGAACTGGCGCTGAATGTGTGTCAGTGGCGGATACAGCGGTCTCTGTTT 235

QY 66 ProTyrArgCysAspLeuSerAsnGluAspIleLeuSerMetPheSerAlaIleArg 85

Db 236 CCATATAAATGTATCTTTTCAGTAGAGGATGAAGTTTGTCCATGTCTCTCGATTAAG 295

QY 86 SerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThr 105

Db 296 GCTCAACATAAAGGTGTGTATGTGTCAATTAATATGTCTGTGTTAGCTCTGCCAGAGCCT 355

QY 106 LeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnValAsnValLeuAlaLeu 125

Db 356 CTGTTGAACGGCAACCCAGCGCTGGAGCACTATGATGAACGTGAATTAATTGGCCCTG 415

QY 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145

Db 416 TCATTGTGCACCGCTGAGGCTTTCAGTCCATGAAAGAAAGAAATATTGATGGCCAT 475

QY 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165

Db 476 ATCATTAATTAACAGTATGTCGGCATCGGTTGTAACACAGTGCCTATACACACTTC 535

QY 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnLeuArg 185

Db 536 TACACCGCTACTAATACGAGTGACTGCTCTCACCGAAGGTTTGAGGCAAGATTACGA 595

QY 186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGluThr 203

Db 596 GAGGCCAAACCCACATACGTGACAGTATATATATATATATATATATATATATATATAT 649

RESULT 50

CA474613

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CA474613 863 bp mRNA linear EST 12-NOV-2002

AGENCOURT 10700406 NCI CGAP ZKId1 Danio rerio cDNA clone

IMAGE:6796850 5', mRNA sequence.

CA474613

CA474613.1 GI:24930965

EST.

Danio rerio (zebrafish)

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 863)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: CGAPbs-r@mail.nih.gov

Tissue Procurement: Leonard I. Zon, M.D.

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM14309 row: d column: 01

High quality sequence stop: 635.

Location/Qualifiers

1. .863

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="IMAGE:6796850"

/lab_host="DH10B (T1-resistant)"

/clone_lib="NCI CGAP ZKId1"

/note="Organ: kidney; Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 Kb. Constructed by J. Wang (Research Genetics, Invitrogen Corp) from tissue donated by L. Zon (Harvard University). Note: this is a NCI CGAP Library."

ORIGIN

Alignment Scores:

Fri Sep 17 09:20:50 2004

Pred. No.: 7.6e-80 Length: 863
 Score: 785.00 Matches: 144
 Percent Similarity: 86.83% Conservative: 34
 Best Local Similarity: 70.24% Mismatches: 26
 Query Match: 58.71% Indels: 1
 DB: 14 Gaps: 0

US-10-063-735-128 (1-260) x CA474613 (1-863)

QY	57	SerAlaGlyTyrProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluasp	76
Db	1	AGTGGAGGACTCAGCGGTGCTCTTTCCATATAAATGTGACCTTCAGTAGAGGATGAA	60
QY	77	IleLeuSerMetPheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsn	96
Db	61	GTTTTGTCATGTTCTCTCGATTAGGCTCAACATAAGGGTGTGATGTGTGATTAAT	120
QY	97	AsnAlaGlyLeuAlaArgProAspThrLeuSerGlySerThrSerGlyTyrIleAsp	116
Db	121	AATGCTGTTTAGCTCTGCCAGAGCCTCTGTTGAACGGCAAAACAGCGGTGGAGGACT	180
QY	117	MetPheAsnValAsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMet	136
Db	181	ATGATGAACGTGAATGTAATTGGCTGGCAGTGTGCACCCGTGAGGCTTACCACTCCATG	240
QY	137	LysGluArgAsnValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArg	156
Db	241	AAAGAAGAATAATTGATGATGGCCATATCATTAATTAACAGTATGCTGGGCATCGG	300
QY	157	ValLeu-ProLeuSerValThrHisPheTyrSerAlaThrIleValAlaValThrAlaLe	176
Db	301	GTTGTAAACAGTGGCTTTTACACACTTCTACACCGCTACTAAATACGCGAGTACTGCTCT	360
QY	176	uThrGluGlyLeuArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIle	196
Db	361	CACCGAAGGTTTGAGGCAAGATTACGAGAGGCCAAACCCACATACGTGCCACAAGTAT	420
QY	196	eSerProGlyValValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluIly	216
Db	421	ATCCCTTGTTTGTGGAGACAGAAATTTGCCCTACAGACTTTTGTGTAACCAAGACAA	480
QY	216	sAlaAlaAlaThrTyrGluGlnMetLysCysIleuLysProGluAspValAlaGluAlaVa	236
Db	481	GGCTTCTGCCACCTACAAAGATATAAAGTGCTGAGCCAGAGATCTAGCAATGTCAGT	540
QY	236	IleTyrValLeuSerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProTh	256
Db	541	GGTTTATGTCCTTAGCGCTCCTCTCATGTTCAATTTGGTACATTCAGATGAGACCTGT	600
QY	256	rGluGlnValThr	260
Db	601	GGAACAGCTGACA	613

Search completed: September 16, 2004, 18:36:46
 Job time : 2478 secs

C	78	421.8	28.0	897	13	BX777216	BX777216 BX777216
	79	420.4	27.9	963	12	BG528781	BG528781 602580128
	80	419.8	27.9	580	14	CA779637	CA779637 MPL384.1
	81	402.8	26.8	977	13	BUB39980	BUB39980 AGENCOURT
	82	399.4	26.5	554	10	BE031247	BE031247 129747 MA
	83	395.6	26.3	413	9	AA575928	AA575928 nm56b12.s
	84	394.4	26.2	398	9	AI200014	AI200014 qf90d03.x
	85	394	26.2	678	12	BI391549	BI391549 pcpin.pk0
	86	392.4	26.1	408	9	AA809706	AA809706 nk96f06.s
	87	389	25.8	389	9	AI620164	AI620164 tu46c12.x
	88	387.4	25.7	390	12	BG983161	BG983161 IL5-CN006
	89	387	25.7	489	12	BG717600	BG717600 602698216
	90	386	25.6	769	14	CF221812	CF221812 AGENCOURT
	91	384.4	25.5	461	12	BM088288	BM088288 S01723 MA
	92	379.6	25.2	539	12	BG488598	BG488598 602534511
	93	377.2	25.1	388	12	BQ011157	BQ011157 UI-1-BC1P
	94	376.2	25.0	538	13	BX111640	BX111640 BX111640
	95	370	24.6	379	9	AI221658	AI221658 qg93d04.x
	96	368.8	24.5	385	12	BM681153	BM681153 UI-E-EJ0-
	97	366	24.3	507	9	AI930229	AI930229 ul62a03.Y
	98	366	24.3	849	13	B0212233	B0212233 603950353
	99	359	23.9	374	12	BM674861	BM674861 UI-E-EJ0-
	100	357.8	23.8	672	14	CD469548	CD469548 LeukoS2_4

RESULT 1	822 bp	mRNA	linear	EST 15-MAY-2001
LOCUS	BG741589	602635416F1 NCI_CGAP_Skn3 Homo sapiens cdna clone IMAGE:4780659 5',		
DEFINITION	mRNA sequence.			
ACCESSION	BG741589	1 GI:14052242		
VERSION	BG741589			
KEYWORDS	EST.			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens (human)			
REFERENCE	NIH-MGC http://mgi.nci.nih.gov/.			
AUTHORS	Contact: Robert Strausberg, Ph.D.			
JOURNAL	Tissue Procurement: James Cleaver, M.D.			
COMMENT	CDNA Library Preparation: Life Technologies, Inc.			
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA			
	Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LLNL at:			
	http://image.llnl.gov			
	Plate: LLAM10639 row: p column: 04			
	High quality sequence stop: 803.			
FEATURES	Location/Qualifiers			
source	1..822			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:4780659"			
	/lab_host="DH10B (T1 phage-resistant)"			
	/clone_lib="NCI_CGAP_Skn3"			
	/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;			
	Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.			
	Average insert size 1.5kb. Library constructed by Life			
	Technologies. Note: this is a NCI_CGAP Library."			

ORIGIN	51.3%; Score 772.4; DB 12; Length 822;
Query Match	Best Local Similarity 99.5%; Pred. No. 1.9e-126;
Matches 806; Conservative	0; Mismatches 1; Indels 3; Gaps 3;

RESULT 2	829 bp	mRNA	linear	EST 27-FEB-2001			
LOCUS	BG324477	602422421F1 NIH_MGC_14 Homo sapiens cdna clone IMAGE:4560485 5',					
DEFINITION	mRNA sequence.						
ACCESSION	BG324477	1 GI:13130914					
VERSION	BG324477						
KEYWORDS	EST.						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
REFERENCE	1 (bases 1 to 829)						
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
JOURNAL	NIH-MGC http://mgi.nci.nih.gov/.						
	National Institutes of Health, Mammalian Gene Collection (MGC)						
	Unpublished (1999)						

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DTP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LLCM1269 row: j column: 06
 High quality sequence stop: 755.

FEATURES

source

1..829
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4560485"
 /tissue_type="renal cell adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 14"
 /note="Organ: kidney; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dr priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACACAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 50.7%; Score 763.2; DB 12; Length 829;
 Best Local Similarity 97.2%; Pred. No. 7,8e-125;
 Matches 808; Conservative 0; Mismatches 19; Indels 4; Gaps 3;
 45 GCCGGCGCTCAGCTCTCGACCCCGCTGTGGGTAGTCCACGAGCGGACGGCGCGG 104
 Db 1 GCCGGCGCTCAGCTCTCGACCCCGCTGTGGGTAGTCCACGAGCGGACGGCGCGG 60
 105 TGGGCCCATGTCGACGGCCGCGATGAGCGGTGGCGGACCGGCTGGCGTGGTACCGG 164
 Db 61 TGGGCCCATGTCGACGGCCGCGATGAGCGGTGGCGGACCGGCTGGCGTGGTACCGG 120
 165 GGCTCTGGGGGGGATCGGGCGGGCGCTGGCCCGGGCCCTGTCCAGCAGGCACTGAAGT 224
 Db 121 GGCTCTGGGGGGGATCGGGCGGGCGCTGGCCCGGGCCCTGTCCAGCAGGCACTGAAGT 180
 225 GGTGGGCTGGCCCGGCTGTGGGCAACATCGAGAGCTGCTGCTGAATGAAGATGC 284
 Db 181 GGTGGGCTGGCCCGGCTGTGGGCAACATCGAGAGCTGCTGCTGAATGAAGATGC 240
 285 AGGCTACCCCGGACTTTGATCCCTACAGATGTGACCTATCAATGAAGAGCATCCT 344
 Db 241 AGGCTACCCCGGACTTTGATCCCTACAGATGTGACCTATCAATGAAGAGCATCCT 300
 345 CTCATGTTCTCAGTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGC 404
 Db 301 CTCATGTTCTCAGTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGC 360
 405 TGGCTTCGGCCGGCTCAGACCCCTGCTCTCAGGAGCAGCAGTGGTGGAGGACATGTT 464
 Db 361 TGGCTTCGGCCGGCTCAGACCCCTGCTCTCAGGAGCAGCAGTGGTGGAGGACATGTT 420
 465 CAATGTGAACGTGTGGCCCTCAGCATCTGCACACGGGAGCCCTACAGTCCATGAAGGA 524
 Db 421 CAATGTGAACGTGTGGCCCTCAGCATCTGCACACGGGAGCCCTACAGTCCATGAAGGA 480
 525 GCGGAATGTGGAACGATGGGACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGT 584
 Db 481 GCGGAATGTGGAACGATGGGACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGT 540
 585 ACCCGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGTGCACAGA 644
 Db 541 ACCCGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGTGCACAGA 600

645 GGGCTGAGGCAAGAGCTTCGGGAGGCCAGCCACATCCGAGCCACGTCATCTCTCC 704
 Db 601 GGGCTGAGGCAAGAGCTTCGGGAGGCCAGCCACATCCGAGCCACGTCATCTCTCC 660
 705 AGGTGTGTGGGAGA-CACAAATTCGCTTCAAACTCCACGACAGGACCCCTGAGAAGGCGAG 763
 Db 661 AGGTGTGTGTGGGAGACCACAAATTCGCTTCAAACTCCACGACAGGACCCCTGAGAAGGCGAT 720
 764 CTGCCACCTATGAGCAAAATGAAGTGTCTCAAAACCGGAGGATGTGCCGAGGCTGTATCT 823
 Db 721 CTG-CANCTATGAGCAAAATGAAGTGTCTCAAAACCGGAGGATGTGCCGAGGCTGTATCT 779
 824 ACGTCTCAGCACCCCGCCGACATCCAGATTGGAGACATCCAGATGAGGC 874
 Db 780 ACGTC-TCAGCACCCCGGACATTCGATTGGGGACTTCCGATGAAGGC 828

RESULT 3
 BM471232
 LOCUS
 DEFINITION 1010 bp mRNA linear EST 05-PEB-2002
 AGENCOURT 6478395 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5563124
 5', mRNA sequence.
 ACCESSION BM471232
 VERSION BM471232.1 GI:18520274
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1010)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12293 row: j column: 21
 High quality sequence stop: 561.

FEATURES
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 1..1010
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5563124"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_72"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

ORIGIN
 Query Match 48.7%; Score 732.4; DB 12; Length 1010;
 Best Local Similarity 92.2%; Pred. No. 2.1e-119;
 Matches 828; Conservative 0; Mismatches 61; Indels 9; Gaps 5;
 38 GAGAGCGCGCGGCTCAGCTCTCCACCCCTGTGGCTAGTCCAGGAGCGGACG 97
 Db 13 GAGAGCGCGCGGCTCAGCTCTCCACCCCTGTGGCTAGTCCAGGAGCGGACG 72
 98 GCGGGGTGGGCGCATGCGCAGCCCGGATGAGCGGTGGCGACCGGCTGGCGCTGG 157
 Db 73 GCGGGGTGGGCGCATGCGCAGCCCGGATGAGCGGTGGCGACCGGCTGGCGCTGG 132
 158 TGACGGGGGCTGGGGGGCATGCGCGCGCGCTGGCGCGCCCTGGTCCAGGAGGAC 217


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676 ACCACATCCGAGCAGCGTCATCTCTCCAGGTGT-GTGGAGACACAAATTCGCTTCAA 734
661 ACCACATCCGAGCAGCGTCATCTCTCCAGGTGTGGTGGAGACAAATTCCTTCAA 720
735 ACTCCAGCA-CAAGACCCCTGGAAGGAGC--TGCCACCTATGAGCAAAATGAAGTGTCT 791
721 ACTCCAGCAGGAGCAGCGTCTGAGAGGAGCAGCTGGCCCCCTATGAACAAATGAAGTGTCC 780
792 CAACCCGAGGATGTG 807
781 TCACACCCAGGAATG 796

RESULT 5
BI818880
LOCUS
DEFINITION
603037354F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178397 5',
mRNA sequence.
ACCESSION
BI818880
VERSION
BI818880.1 GI:15930430
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 940)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11444 row: 1 column: 14
High quality sequence stop: 781.
FEATURES
source
1..940
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5178397"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/notes="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 Kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 46.6%; Score 701.4; DB 12; Length 940;
Best Local Similarity 93.6%; Pred. No. 6.5e-114;
Matches 864; Conservative 0; Mismatches 41; Indels 18; Gaps 12;

QY 1 CGCGGATCGACCAACAGCAGTC-GGCGGCGGCGGAGAGAGCGGCGGCGGTGAGCTC 59
Db |||||
15 CGCGGATTCGACCAACAGCAGTC-TGGCGGCGGCGGAGAGAGCGGCGGCGGTGAGCTC 74
QY |||||
60 CTCGACCCCGTGTGCGGGCTAGTCCAGAGGCGGAGCGGCGGCGGTGGCGCCATGCCAG 119
Db |||||
75 CTCGACCCCGTGTGCGGGCTAGTCCAGAGGCGGAGCGGCGGCGGTGGCGCCATGCCAG 134
QY |||||
120 GCCCGGATGAGCGGTGGCGGAGCCGCTGGCGCTG-GTGACGGGCGGCGTGGGGGG-- 176

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Db |||||
135 GCCCGGATGAGCGGTGGCGGAGCCCGCTGGCGTGTGTGACGGGGGCTCGGGGTGGC 194
QY |||||
177 -CATCGGCGCGGCGGTGGCCC-GGGCCCTGGTCCAGCAGGAGCTCAAGGTGTGGGCTGC 234
Db |||||
195 ATCTGGCTGGCGCGTGGCCCTGGTCCAGCAGGAGCTGAAGGTGTGGGCTGC 254
QY |||||
235 GCCGCACTGTGGGCAACATCGAGGAGCTGGCTGTGAATGTAAGAGTGCAGGCTACCCC 294
Db |||||
255 GCCGCACTGTGGGCAACATCGAGGAGCTGGCTGTGAATGTAAGAGTGCAGGCTACCCC 314
QY |||||
295 GGGACTTTGATCCCTCAGATGTGCTATCAATGAAGAGGACATCTCTCCATGTTC 354
Db |||||
315 GGGACTTTGATCCCTCAGATGTGCTATCAATGAAGAGGACATCTCTCCATGTTC 374
QY |||||
355 TCAGCTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTGCC 414
Db |||||
375 TCAGCTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTGCC 434
QY |||||
415 CGGCTGAC-ACCTGTCTCTCAGCAGCACCAAGTGTGGAGGACATGTTCAAT--GTG 471
Db |||||
435 CGGCTGACAAACCTGTCTCTCAGCAGCACCAAGTGTGGAGGACATGTTCAATGTGA 494
QY |||||
472 AACGTGTGSCCTCAGCATCTGCACGCGGAGCCTACCACTCAACAATGCTGGCTTGCC 531
Db |||||
495 AGTTGTGCTGGCCCTCAGCATCTGCACGCGGAGCCTACCACTCAACAATGAGGAGCG 554
QY |||||
532 GTGACGATGGGACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
Db |||||
555 GTGACGATGGGACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 614
QY |||||
592 TCTGTGACCACTTCTATAGTGCCACCAAGTATGCCCTCACTGCGTGCAGAGGAGTGC 651
Db |||||
615 TCTGTGACCACTTCTATAGTGCCACCAAGTATGCCCTCACTGCGTGCAGAGGAGTGC 674
QY |||||
652 AGGCAAGAGCTTGGGAGGCGGAGCCACATCGAGCCACGTC-ATCTCTCCAGTGT 710
Db |||||
675 AGGCAAGAGCTTGGGAGGCGGAGCCACATCGAGCCACGTC-ATCTCTCCAGTGT 734
QY |||||
711 GGTGGAGAC-ACAAATTCGCTTCAAACTCCACGACAGGAGCCCTGAGAGGAGCTGCCA 769
Db |||||
735 GGGGAGACAAACAATTCGCTTCAAACTCCACGACAGGAGCCCTGAGAG--CAGTGGCA 792
QY |||||
770 CCTATGAGCAAAATGAA-GTGTCTCAAAACCGAGAGATGGCCGAGGCTGTATCTACGTC 828
Db |||||
793 CCTATGAGCAAAATGAAAGGTGGCTCAAAACCGAGGATGGCCGAGGCTGTATCTACGTA 852
QY |||||
829 CTCAGCACCCCGCACACATCCAGATTCAGATTCAGATGAGGCCACGAGGAGGAGTGT 888
Db |||||
853 CTCAGACCC---TGAACAATCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 908
QY |||||
889 ACCTAGTGTGAGTGGGAGTCTCT 911
Db |||||
909 ACATAGTGTGAGTGGGAGTCTCT 931

RESULT 6
BE796469
LOCUS
DEFINITION
601589817F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943948 5',
mRNA sequence.
ACCESSION
BE796469
VERSION
BE796469.1 GI:10217667
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1063)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

```

QY	597	GA	CCCACTTCTATAGTGGCCACCAAGTATGCGGTCACTTGGCTCAGACAGGGAC-TGAGGC	655
Db	622	GA	-CCAAATTTCTATAGTGGCCA-CAAGTATGCCGTCATCTGCTGACAGAGCACTTGAGGC	679
QY	656	AAGAGCTTCGGGAGGCCACAGACCCACATCCGAGCCACGTGCA-TCTTCCAGGTGTGGTG	714	
Db	680	AAGAGCTTCGGGAGGCCAAGACCCACATCCGAGCCACGTGCAATTTCTCCAGGTGTGGTG	739	
QY	715	GAGACACAATTCGCTTTAAACTCCACGACAGAGACCTTGAGAAGGACAGTGCACCTAT	774	
Db	740	GAGACACAATTCGCTTTAAAGTCCCA-GACAAGGACCTTGAGAAGGCACTTGCACTAT	798	
QY	775	GAGCAATGAGTGTCTCAAAACCGAGGATGTGGCGAGGCTGTATCTA--GTCCTCA	832	
Db	799	AAGCAATGAGTGGTTTTAAACCCGAGAATTTGCCGAGGATGGAAATTAAGGTCATCA	858	
QY	833	GCACCCCGGCACATCCAGATTGGAGACATCCAGATGAGGCCACGAGACAGGTGACCT	892	
Db	859	GAAACCCCGCAAGATTCGGAATGTGGAAATTCACAATAATGTCACGAGAGCGGACCT	918	
QY	893	AGTACTGTGGAGCTCTCTTCCCTCCCAACCCCTCATGGCTGCGCTC	942	
Db	919	ACGACCGTGGGAAGCCCATATATATCCACCACTATGAGGGTGAACGC	968	
RESULT 7				
BF979853/c				
LOCUS				
DEFINITION				
BF979853				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
<p>NIH-MGC http://mgc.nci.nih.gov/.</p> <p>National Institutes of Health, Mammalian Gene Collection (MGC)</p> <p>Unpublished (1999)</p> <p>Contact: Robert Strausberg, Ph.D.</p> <p>Email: gsapsb@mail.nih.gov</p> <p>Tissue Procurement: Miklos Palkovits, M.D., Ph.D.</p> <p>cdna Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshuyuki and Piero Carninci (RIKEN)</p> <p>cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)</p> <p>DNA Sequencing by: Incyte Genomics, Inc.</p> <p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov</p> <p>Plate: L1AM10037 row: 9 column: 17</p> <p>High quality sequence start: 24</p> <p>High quality sequence stop: 679.</p> <p>Location/Qualifiers</p> <p>1..679</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="IMAGE:4374184"</p> <p>/lab_host="DH10B"</p> <p>/clone_lib="NIH_MGC_97"</p> <p>/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtagag); Oligo-dt primed using primer_5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI). National Institutes of Health. This is a NIH_MGC Library."</p>				
FEATURES				
source				

Query Match 43.8%; Score 659; DB 10; Length 679;
Best Local Similarity 100.0%; Pred. No. 21e-106;
Matches 659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	767	CCACCTATGAGCAATGAAGTCTCTCAAAACCGAGGATGCGCGAGGCTGTATCTACG	826
DB	679	CCACCTATGAGCAATGAAGTCTCTCAAAACCGAGGATGCGCGAGGCTGTATCTACG	620
QY	827	TCCTCAGACACCCCGCACACATCCAGATGGAGATCCAGATGAGGCCACCGAGCAGG	886
DB	619	TCCTCAGACACCCCGCACACATCCAGATGGAGATCCAGATGAGGCCACCGAGCAGG	560
QY	887	TGACCTAGTGAAGTGGGAGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC	946
DB	559	TGACCTAGTGAAGTGGGAGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC	500
QY	947	CTCTGGATTTAGTGTGATTTCTGGATTCAGGATACCACTTCTCTGTCACACCCCGA	1006
DB	499	CTCTGGATTTAGTGTGATTTCTGGATTCAGGATACCACTTCTCTGTCACACCCCGA	440
QY	1007	CCAGGGCTAGAAAATTTGTTGAGATTTTATATCATCTTGTCAAAATGCTTCAGTTGT	1066
DB	439	CCAGGGCTAGAAAATTTGTTGAGATTTTATATCATCTTGTCAAAATGCTTCAGTTGT	380
QY	1067	AAATGTGAAAATGGGCTGGGGAAGAGGTGCTCCCTAAATGCTTTACTTGTAACT	1126
DB	379	AAATGTGAAAATGGGCTGGGGAAGAGGTGCTCCCTAAATGCTTTACTTGTAACT	320
QY	1127	TGTTCTTGTGCCCCGTCAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	1186
DB	319	TGTTCTTGTGCCCCGTCAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	260
QY	1187	GGAAGAGAGTGTGCGCAAAATCCCATCTTCTTGACACTCAAGTCTGTGGCTCAGGGC	1246
DB	259	GGAAGAGAGTGTGCGCAAAATCCCATCTTCTTGACACTCAAGTCTGTGGCTCAGGGC	200
QY	1247	TGGGGTGGCAGAGGAGGCTTCACTTATATCTGTGTGTATATCCAGGGCTCCAGACTT	1306
DB	199	TGGGGTGGCAGAGGAGGCTTCACTTATATCTGTGTGTATATCCAGGGCTCCAGACTT	140
QY	1307	CTCTCTGCTGCCCCGTCAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	1366
DB	139	CTCTCTGCTGCCCCGTCAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	80
QY	1367	GCCAGAGTGGCTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1425
DB	79	GCCAGAGTGGCTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	21

RESULT 8
BU624717/c
LOCUS
DEFINITION
UI-H-FGI-bgi-h-13-0-UI.s1 NCI CGAP FGI Homo sapiens cDNA clone
UI-H-FGI-bgi-h-13-0-UI 3', mRNA sequence.
BU624717
BU624717.1 GI:23290932
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 672)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
Tumor Gene Index
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA sequencing by: Dr. M. Bento Soares, University of Iowa

FEATURES
source

1..672
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FGI-bgi-h-13-0-UI"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FGI"
/note="Organ: Enchondroma; Vector: pT73-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FGI is a normalized cDNA library obtained from a
pool of mRNA from 2 cell lines from Enchondroma tissues.
The library was constructed according to Bonaldo, Lemmon
and Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT73-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is CGGTCACTC. The cell lines were provided by Dr.
James Martin from the University of Iowa.
TAG TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
TAG_Lib=UI-H-FGI
TAG_SEQ=CGGTCACTC"

ORIGIN

Query Match	43.6%;	Score 656.4;	DB 13;	Length 672;
Best Local Similarity	99.1%;	Pred. No. 6e-106;		
Matches 660;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
QY	840	CGCACACATCCAGATTTGGAGACATCCAGATGAGGCCACGGAGCAGGTGACCTAGTGACT	899	
Db	672	CGCACACATCCAGATTTGGAGACATCCAGATGAGGCCACGGAGCAGGTGACCTAGTGACT	613	
QY	900	GTGGGAGCTCTCTCC		

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Qy 1380 TTCTGTCCCTCTCTGGGTCATCCCTCCACTCTGACTCTGACTATGAGCAGACAC 1439
Db 132 TTCTGTCCCTCTCTGGGTCATCCCTCCACTCTGACTCTGACTATGAGCAGACAC 73
Qy 1440 AGGCGCTGGCCATGATTTCAATGGTGCATTTAAATAAGAAAAAATCGCAACAAAA 1499
Db 72 AGGCGCTGGCCATGATTTCAATGGTGCATTTAAATAAGAAAAAATCGCAACAAAA 13
Qy 1500 AAAAAA 1505
Db 12 AAAAAA 7

RESULT 9
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LOCUS 602402863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4545231 5',
DEFINITION mRNA sequence.
ACCESSION BG282361
VERSION BG282361.1 GI:13031288
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 852)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW1229 row: n column: 16
High quality sequence stop: 851.
Location/Qualifiers
1..852
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4545231"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_20"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGACAGG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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ORIGIN

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Query Match 43.2%; Score 650; DB 12; Length 852;
Best Local Similarity 98.1%; Pred. No. 7.9e-105;
Matches 689; Conservative 0; Mismatches 10; Indels 3; Gaps 3;

Qy 1 CGCGGATCGACCCACAGCAGGTCCGCGCGGCGGAGAGAGCGCGCGGTCACTCC 60
Db 12 CGCGGATCGACCCACAGCAGGTCCGCGCGGCGGAGAGAGCGCGCGGTCACTCC 71
Qy 61 TCGACCCCGTGTCCGGCTAGTCCAGCGAGGCGGCGGCGGTCCATGGCCAGG 120
Db 72 TCGACCCCGTGTCCGGCTAGTCCAGCGAGGCGGCGGCGGTCCATGGCCAGG 131
Qy 121 CGCGGATCGACCGGTGGCGCGACCGGCTGGCTGGTACGGGGGCTCGGGGGCATC 180
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Db 132 CC CGGATGAGCGGTGGCGCGACCCGGCTGGCGTGGTGAACGGGGGCTCGGGGGGCATC 191
Qy 181 GGCGCGCGCTGGCCCGGGCCCTGGTCCAGCAGGACTGAAGTGGTGGGTGCGCCGC 240
Db 192 GGCGCGCGCTGGCCCGGGCCCTGGTCCAGCAGGACTGAAGTGGTGGGTGCGCCGC 251
Qy 241 ACTGTGGGCAACATCGAGGAGCTGGCTGTCTGAATGTAAAGTGCAGGCTACCCCGGACT 300
Db 252 ACTGTGGGCAACATCGAGGAGCTGGCTGTCTGAATGTAAAGTGCAGGCTACCCCGGACT 311
Qy 301 TTGATCCCTACAGATGTGACCTATCAAAATGA-AGAGGACATCTCTCCATGTTCTCAGC 359
Db 312 TTGATCCCTACAGATGTGACCTATCAAAATGACCGAGGACATCTCTCCATGTTCTCAGC 371
Qy 360 TATCCGTTCAGCAGCGGTGTAGACATCTGATCAACATGCTGGCTTGGCCCGGCC 419
Db 372 TATCCGTTCAGCAGCGGTGTAGACATCTGATCAACATGCTGGCTTGGCCCGGCC 431
Qy 420 TGACACCTGTCTCTCAGCAGCACCAGTGGTTGGAAGGACATGTTCAATGTGAACGTGC- 478
Db 432 TGACACCTGTCTCTCAGCAGCACCAGTGGTTGGAAGGACATGTTCAATGTGAACGTGC 491
Qy 479 TGGCCCTCAGCATCTGCACACGGGAAGCCTACCACTGCTGACAGAGGAGCTGAGGCAAG 538
Db 492 TGGCCCTCAGCATCTGCACACGGGAAGCCTACCACTGCTGACAGAGGAGCTGAGGCAAG 551
Qy 539 ATGGGCACATCAATTAACATCAATGATGATGCTGGCCACCGAGTGTACCCCTGCTGTGA 598
Db 552 ATGGGCACATCAATTAACATCAATGATGATGCTGGCCACCGAGTGTACCCCTGCTGTGA 611
Qy 599 CCCACTTCTATAGTGGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGAGCTGAGGCAAG 658
Db 612 ACCACTTCTATAGTGGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGAGCTGAGGCAAG 671
Qy 659 AGCTTCGGAGGCGGCCAGA-CCACATCCGAGCGCCAGCTGCATC 699
Db 672 AGCTTCGGAGGCGGCCAGAGCCCAATCCGAGCGCAAGTGTCTC 713

RESULT 10
AL568188/c
LOCUS AL568188 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF035YM23 3-PRIME, mRNA sequence.
ACCESSION AL568188
VERSION AL568188.2 GI:31291036
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 980)
Li.W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12922282.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8845.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF035AG12NP1&cluster=8845.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF035AG12NP1.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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FEATURES

source


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/clone="CS0DF035YM23"
/tissue_type="FETAL BRAIN"
/dev stage="fetal"
/clone lib="Homo sapiens FETAL BRAIN"
/notes="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN
Query Match 42.8%; Score 644.8; DB 9; Length 980;
Best Local Similarity 98.3%; Pred. No. 6.5e-104;
Matches 644; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 785 AGTGTCTCAAAACCCGAGGATGTGGCGAGCTGTATCTACCTCTCAGCAGCCCGGCAC 844
Db 709 AGTGTCTCAAAACCCGAGGATGTGGCGAGCTGTATCTACCTCTCAGCAGCCCGGCAC 650
QY 845 ACATCCAGATTGGAGACATCCAGATGAGGCCACGAGCAGCTGACCTAGTACTGTGG 904
Db 649 ACATCCAGATTGGAGACATCCAGATGAGGCCACGAGCAGCTGACCTAGTACTGTGG 590
QY 905 AGCTCTCTCTCCCTCCCGACCTTCATGGCTTGCCTCTGCTCTGGATTTTAGGTGT 964
Db 589 AGCTCTCTCTCCCTCCCGACCTTCATGGCTTGCCTCTGCTCTGGATTTTAGGTGT 530
QY 965 GATTTCTGGATCAGCGATACACCTCTCTGCTCCACCCGACGAGGCTGAGAAAATTT 1024
Db 529 GATTTCTGGATCAGCGATACACCTCTCTGCTCCACCCGACGAGGCTGAGAAAATTT 470
QY 1025 GTTTGAGATTTTATATCATCTTGTCAAAATTCCTCAGTTGTAATGTGAAAATGGGCT 1084
Db 469 GTTTGAGATTTTATATCATCTTGTCAAAATTCCTCAGTTGTAATGTGAAAATGGGCT 410
QY 1085 GGGGAAAGAGGTGTGCTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTT 1144
Db 409 GGGGAAAGAGGTGTGCTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTT 350
QY 1145 CACTTGGCTTTGCTGCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCT 1204
Db 349 CACTTGGCTTTGCTGCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCT 290
QY 1205 AAATCCCATCTTCTTGACCTCAACGCTCTGCTCAGGCTGGGTTGGCAGAGGAGG 1264
Db 289 AAATCCCATCTTCTTGACCTCAACGCTCTGCTCAGGCTGGGTTGGCAGAGGAGG 230
QY 1265 CCCTTCACTTATATCTGTTGTTATCCAGGCTCCAGACTTCCTCTGCTGCCCCA 1324
Db 229 CCCTTCACTTATATCTGTTGTTATCCAGGCTCCAGACTTCCTCTGCTGCCCCA 170
QY 1325 CTGACCTCTCCCTTTATCTATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 1384
Db 169 CTGACCTCTCCCTTTATCTATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 110
QY 1385 GTCCCTCTTGGGTCATCCCTCCACTCTGACTCTGACTTGGCAGCAGAACACC 1439
Db 109 GTCCCTCTTGGGTCATCCCTCCACTCTGACTCTGACTTGGCAGCAGAACACTNC 55

RESULT 11
CB851997/c
LOCUS
DEFINITION CB851997 669 bp mRNA linear EST 22-APR-2003
UI-CF-FNO-aes-e-22-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
CB851997 UI-CF-FNO-aes-e-22-0-UI 3', mRNA sequence.
VERSION CB851997
KEYWORDS CB851997.1 GI:30046840
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 669)
```

AUTHORS
TITLE

Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-38, >POLY A#Simple_repeat (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..669
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FNO-aes-e-22-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="DHI0B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FNO"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (ENI and
DUI) The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_SEQ=None found"

ORIGIN

Query Match 42.5%; Score 639.4; DB 14; Length 669;
Best Local Similarity 99.5%; Pred. No. 6e-103;
Matches 662; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
QY 841 GCACATCCAGATTGGAGACATCCAGATGAGGCCACGAGCAGGTGACCTAGTACTG 900
Db 669 GCACATCCAGATTGGAGACATCCAGATGAGGCCACGAGCAGGTGACCTAGTACTG 610
QY 901 TGGAGCT 960
Db 609 TGGGA-CT 551
QY 961 TGTGATTTCTGGATCAGCGGATACCACTTCCTGTCCACACCCCGACAGGCGGTAGAAA 1020
Db 550 TGTGATTTCTGGATCAGCGGATACCACTTCCTGTCCACACCCCGACAGGCGGTAGAAA 491
QY 1021 ATTGTTTGGATTTTATATCATCTGTCAAAATTCCTCAGTTGTAATGTGAAAATG 1080
Db 490 ATTGTTTGGATTTTATATCATCTGTCAAAATTCCTCAGTTGTAATGTGAAAATG 431
QY 1081 GGCTGGGAAAGAGGTGTGTCCTCAATTTTAACTTTTAACTTTTAACTTTTAACTTTT 1140
Db 430 GGCTGGGAAAGAGGTGTGTCCTCAATTTTAACTTTTAACTTTTAACTTTTAACTTTT 371
QY 1141 TGGGCACTTGGCCCTTTGTCTGTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGTTGTG 1200
Db 370 TGGGCACTTGGCC-TTCTCTCTCTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGTTGTG 312
QY 1201 GCCAAATCCCATCTCTCTTGGACCTCAAGCTCTGCGCTGAGGCTGGGCTGGCAGAGG 1260

Db 311 GCACAAATCCCACTCTTCTTGACCTCAAGTCTGTGGCTCAGGCTGGGTGCAGAGG 252
 QY 1261 GAGCCCTTCACTTATATCTGTGTGTATCCAGGGCTCCAGACTTCTCTCTGCTGC 1320
 Db 251 GAGCCCTTCACTTATATCTGTGTGTATCCAGGGCTCCAGACTTCTCTCTGCTGC 192
 QY 1321 CCACCTGACCTCTCCCTTATCTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
 Db 191 CCACCTGACCTCTCCCTTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 132
 QY 1381 TCTGTCT 1440
 Db 131 TCTGTCT 72
 QY 1441 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 Db 71 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 12
 QY 1501 AAAAA 1505
 Db 11 AAAAA 7

RESULT 12
 BM755987
 LOCUS
 DEFINITION K-EST0034121 S1SNU5 Homo sapiens cDNA clone S1SNU5-38-A10 5', mRNA
 sequence.
 ACCESSION BM755987
 VERSION BM755987.1 GI:19085602
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 640)
 REFERENCE Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 TITLE Unpublished (2002)
 JOURNAL Contact: Kim YS
 COMMENT Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 38 row: A column: 10
 High quality sequence stop: 640.
 Location/Qualifiers
 1..640
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S1SNU5-38-A10"
 /sex="F"
 /tissue_type="Ascites"
 /cell_type="Lymphoblast-like"
 /cell_line="SNU-5"
 /lab_host="Top10F"
 /clone_lib="S1SNU5"
 /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
 Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand

FEATURES

source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S1SNU5-38-A10"
 /sex="F"
 /tissue_type="Ascites"
 /cell_type="Lymphoblast-like"
 /cell_line="SNU-5"
 /lab_host="Top10F"
 /clone_lib="S1SNU5"
 /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
 Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transposition of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 42.4%; Score 638.4; DB 12; Length 640;
 Best Local Similarity 99.8%; Pred. No. 9.1e-103;
 Matches 639; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 350 TGTCTCAGCTATCCGTTCTCAGCACACGCGGTGTAGACATCTGCATCAACAATGCTGCT 409
 Db 1 TGTCTCAGCTATCCGTTCTCAGCACACGCGGTGTAGACATCTGCATCAACAATGCTGCT 60
 QY 410 TGGCCCGGCTGACACCTCTCTCAGGCAGCACAGTGGTGAAGGACATGTTCAATG 469
 Db 61 TGGCCCGGCTGACACCTCTCTCAGGCAGCACAGTGGTGAAGGACATGTTCAATG 120
 QY 470 TGAACGTGCTGGCCTCAGCATCTGCACACGGGAAGCCTACAGTCCATGAAGAGCGGA 529
 Db 121 TGAACGTGCTGGCCTCAGCATCTGCACACGGGAAGCCTACAGTCCATGAAGAGCGGA 180
 QY 530 ATGTGGACGATGGGCACATCAATTAACATAGCATCTTGGCCACCGAGTGTACCCC 589
 Db 181 ATGTGGACGATGGGCACATCAATTAACATAGCATCTTGGCCACCGAGTGTACCCC 240
 QY 590 TGTCTGACCCACTTCTATAGTGGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGAC 649
 Db 241 TGTCTGACCCACTTCTATAGTGGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGAC 300
 QY 650 TGAGCAAGAGCTTCGGGAGGCCACAGCCACATCCAGAGCCACGTCATCTCTCCAGGTG 709
 Db 301 TGAGCAAGAGCTTCGGGAGGCCACAGCCACATCCAGAGCCACGTCATCTCTCCAGGTG 360
 QY 710 TGGTGGAGACAAATTCGCTTCAAACTCCACGACAGGACCCCTGAGAAGGACGCTGCCA 769
 Db 361 TGGTGGAGACAAATTCGCTTCAAACTCCACGACAGGACCCCTGAGAAGGACGCTGCCA 420
 QY 770 CCTATGACCAATGAAGTGTCTCAAAACCGAGGATGTCGCGAGGCTGTATCTACGTCC 829
 Db 421 CCTATGACCAATGAAGTGTCTCAAAACCGAGGATGTCGCGAGGCTGTATCTACGTCC 480
 QY 830 TCAGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACGAGGAGGTGA 889
 Db 481 TCAGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACGAGGAGGTGA 540
 QY 890 CCTAGTACTGTGGAGCTCTCTCTTCCCTTCCCAACCTTATGAGTTCCTCTCTCTCTCT 949
 Db 541 CCTAGTACTGTGGAGCTCTCTCTTCCCTTCCCAACCTTATGAGTTCCTCTCTCTCTCT 600
 QY 950 TGGATTTAGGTGTGATTTCTGGATCAGGGATACCACT 989
 Db 601 TGGATTTAGGTGTGATTTCTGGATCAGGGATACCACT 640

RESULT 13

BM717452
 LOCUS
 DEFINITION UI-E-EJ0-ahn-c-08-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone
 UI-E-EJ0-ahn-c-08-0-UI 5', mRNA sequence.
 ACCESSION BM717452
 VERSION BM717452.1 GI:19030710
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 649)
 REFERENCE Bonaldo,M.F., Lennon,G. and Soares,M.B.
 AUTHORS Normalization and subtraction: two approaches to facilitate gene
 TITLE discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)

BM717452 649 bp mRNA linear EST 28-FEB-2002
 UI-E-EJ0-ahn-c-08-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone
 UI-E-EJ0-ahn-c-08-0-UI 5', mRNA sequence.

MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 The following repetitive elements were found in this cDNA
 sequence: 603-644, >POLY_A\$imple_repeat
 Seq primer: M13 Reverse.

FEATURES

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 1..649
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-E-EJ0-c-08-0-UI"
 /tissue_type="fetal eyes, lens, eye anterior segment,
 optic nerve, retina, Retina Foveal and Macular, RPE and
 Choroid"
 /dev_stages="fetal and adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-E-EJ0"
 /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-E-EJ0 is a subtracted cDNA library constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT7T3-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tags for this library are: fetal eyes,
 AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment,
 AATCCCGCAT; optic nerve, CCATTAAAGTG; retina, CCGCG; Retina
 Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
 library was created for the program, Gene Discovery in the
 Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match 42.1%; Score 633; DB 12; Length 649;
 Best Local Similarity 99.8%; Pred. No. 8.2e-102;
 Matches 633; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 872 GGCCACGGAGCAGTACCTAGTACCTGGGAGCTCCCTCCCTCCACCTTCA 931
 Db 1 GGCCACGGAGCAGTACCTAGTACCTGGGAGCTCCCTCCCTCCACCTTCA 60
 QY 932 TGGCTTCCCTCCCTCCCTAGTATTTAGTGTGATTTCTGGATCAGGATACCATTC 991
 Db 61 TGGCTTCCCTCCCTCCCTAGTATTTAGTGTGATTTCTGGATCAGGATACCATTC 120
 QY 992 CTGTCCACCCCGACCGAGGGCTAGAAAAATTTGTTGAGATTTTATATCATCTTGTCA 1051
 Db 121 CTGTCCACCCCGACCGAGGGCTAGAAAAATTTGTTGAGATTTTATATCATCTTGTCA 180
 QY 1052 AATTGCTTCAGTGTAAATGTGAAAAATGGCTGGGAAAAGGAGTGGTCCCTCAATTG 1111
 Db 181 AATTGCTTCAGTGTAAATGTGAAAAATGGCTGGGAAAAGGAGTGGTCCCTCAATTG 240
 QY 1112 TTTTACTTGTAACTTCTTGTGCCCCCTGGGACCTTGGCCCTTGTCTCTCTCAGTGT 1171
 Db 241 TTTTACTTGTAACTTCTTGTGCCCCCTGGGACCTTGGCCCTTGTCTCTCTCAGTGT 300

QY 1172 CTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCAATCTTCTTGCACCTCAACG 1231
 Db |||||
 301 CTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCAATCTTCTTGCACCTCAACG 360
 QY 1232 TCTGTGGCTCAGGGCTGGGGTGGCAGAGGGAGGCTTGCACCTATATCTGTGTGTATC 1291
 Db |||||
 361 TCTGTGGCTCAGGGCTGGGGTGGCAGAGGGAGGCTTGCACCTATATCTGTGTGTATC 420
 QY 1292 CAGGGCTCCAGACTTCTCTCTGCTGCCACCTGCACCTCTCCCTTATCTATCTC 1351
 Db |||||
 421 CAGGGCTCCAGACTTCTCTCTGCTGCCACCTGCACCTCTCCCTTATCTATCTC 480
 QY 1352 CTTCTCGGCTCCCGAGCCAGCTTGGCTTCTGTGCTCTCTCGGGTGCATCCCTCCACT 1411
 Db |||||
 481 CTTCTCGGCTCCCGAGCCAGCTTGGCTTCTGTGCTCTCTCGGGTGCATCCCTCCACT 540
 QY 1412 CTGACTCTGACTATGGCAGCAGAACACGAGGCCCTGGCCCTGAGTGATTTCACTGTGATCA 1471
 Db |||||
 541 CTGACTCTGACTATGGCAGCAGAACACGAGGCCCTGGCCCTGAGTGATTTCACTGTGATCA 600
 QY 1472 TTAAGAAAAGAAAATCGCAACCAAAAAA 1505
 Db |||||
 601 TTAAGAAAAGAAAATCGCAACCAAAAAA 634

RESULT 14
 BM848012 627 bp mRNA linear EST 06-MAR-2002
 LOCUS K-EST0127637 S13KMS5 Homo sapiens cDNA clone S13KMS5-43-A10 5',
 DEFINITION mRNA sequence.
 ACCESSION BM848012
 VERSION BM848012.1 GI:19204411
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 627)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoseun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsungemail.kr@kribb.re.kr
 Plate: 43 row: A column: 10
 High quality sequence stop: 627.

FEATURES

source
 1..627
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S13KMS5-43-A10"
 /tissue_type="myeloma"
 /cell_line="KMS-5"
 /lab_host="Top10F"
 /clone_lib="S13KMS5"
 /note="Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly
 (A)+ RNA was dephosphorylated with bacterial alkaline
 phosphatase (BAP) and then decapped with tabacco acid
 pyrophosphatase (TAP). The decapped intact mRNA was
 ligated with DNA-RNA linker including EcoR I site by
 treatment of T4 RNA ligase and the first strand cDNA was
 synthesized from oligo dT-selected mRNA by priming with
 dT-tailed vector. The dT-tailed vector was adjusted to
 have about 60nt. The cDNA vector was circularized with E.
 coli DNA ligase after digestion of EcoRI which site is
 also included in vector. An RNA strand converted to a DNA

QY	861	CATCCAGATGAGGCCACCGAGCAGGTGACCTAGTGACT-GTGGGAGCTCTCTCTTCCT	919
Db	3	CATCCAGATGAGGCCACCGAGCAGGTGACCTAGTGACTGTTGGAGCTCTCTCTTCCT	62
QY	920	CCCCACCTTCATGGCTTGCCCTCTGCGCTCTGGATTTTAGGTGTGATTTCTGGATCAG	979
Db	63	CCCCACCTTCATGGCTTGCCCTCTGCGCTCTGGATTTTAGGTGTGATTTCTGGATCAG	122
QY	980	GGATACCACTTCCTGTGCACACCCGACAGGGGCTAGAAAATTTGTTGAGATTTTTAT	1039
Db	123	GGATACCACTTCCTGTGCACACCCGACAGGGGCTAGAAAATTTGTTGAGATTTTTAT	182
QY	1040	ATCATCTTTGTCAAATGCTTCAGTTGTAAATGTGAAAATGGGCTGGGAAAGAGGTGG	1099
Db	183	ATCATCTTTGTCAAATGCTTCAGTTGTAAATGTGAAAATGGGCTGGGAAAGAGGTGG	242
QY	1100	TGTCCTCAATTTGTTTACTTTGTTAACTTTGTTGTCCTCGGGCACTTGGCCCTTTGTC	1159
Db	243	TGTCCTCAATTTGTTTACTTTGTTAACTTTGTTGTCCTCGGGCACTTGGCCCTTTGTC	302
QY	1160	TGCTCTCAGTGTCTTCCTTTTGACATGCGAAAGAGTTGTGGCCAAATCCCACTCTCT	1219
Db	303	TGCTCTCAGTGTCTTCCTTTTGACATGCGAAAGAGTTGTGGCCAAATCCCACTCTCT	362
QY	1220	TGCACCTCAACGTCTGTGGCTCAGGGCTGGGGTGGCAGAGGAGGCCCTTCACCTTATATC	1279
Db	363	TGCACCTCAACGTCTGTGGCTCAGGGCTGGGGTGGCAGAGGAGGCCCTTCACCTTATATC	422
QY	1280	TGTGTTGTTATCCAGGGCTCCAGACTTCCCTCTCTGCTGTCGCCCACTGCACTCTCCCC	1339
Db	423	TGTGTTGTTATCCAGGGCTCCAGACTTCCCTCTCTGCTGTCGCCCACTGCACTCTCCCC	482
QY	1340	CTTATCTATCTCTCTTCGGCTCCCGAGCCAGCTTGGCTTCTGTGCTCCCTCCTGGGT	1399
Db	483	CTTATCTATCTCTCTTCGGCTCCCGAGCCAGCTTGGCTTCTGTGCTCCCTCCTGGGT	542
QY	1400	CATCCTCCACTGACTCTGACTATGTCAGCAGACACACGAGGCCCTGGCCCACTGGATT	1459
Db	543	CATCCTCCACTGACTCTGACTATGTCAGCAGACACACGAGGCCCTGGCCCACTGGATT	602
QY	1460	TCATGGTGATCATTTAAAAGAAAATTCGCAACCAAAAAA	1505
Db	603	TCATGGTGATCATTTAAAAGAAAATTCGCAACCAAAAAA	648
RESULT	19		
LOCUS	BE895089	886 bp	linear
DEFINITION	601436007F1 NIH MGC_72 Homo sapiens cDNA clone IMAGE:3921217 5', mRNA sequence.		EST 20-OCT-2000
ACCESSION	BE895089		
VERSION	BE895089.1	GI:10358131	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 886)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-i@mail.nih.gov Tissue Procurement: ATCC/DCTD/DTF cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9753 row: n column: 02 High quality sequence stop: 589. Location/Qualifiers		
FEATURES			

LOCUS B1464353 757 bp mRNA linear EST 21-AUG-2001
 DEFINITION 60320405F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5269728 5',
 mRNA sequence.
 ACCESSION B1464353
 VERSION B1464353.1 GI:15255009
 KEYWORDS EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 757)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshituki and Piero Carninci (RIKEN)
 DNA Sequencing by: Incyte Genomics, Inc.
 CDNA Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M11680 row: j column: 01
 High quality sequence stop: 707.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5269728"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 97"
 /note="Organ: testis; Vector: pBluescriptR (modified
 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
 gtcgag; Oligo-dT primed using primer
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 insert size 2.2 kb and normalized to R0T 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: this is
 a NIH_MGC Library."
 ORIGIN
 Query Match 40.9%; Score 615.6; DB 12; Length 757;
 Best Local Similarity 98.9%; Pred. No. 9.6e-99;
 Matches 651; Conservative 0; Mismatches 4; Indels 3; Gaps 3;
 QY 1 CGCGGATCGGACCAAGCAGGTGCGCGCGCGGCGGAGAGCGCGCGGCGTCACTCC 60
 DB 54 CGCGGATCGGACCAAGCAGGTGCGCGCGCGGCGGAGAGCGCGCGGCGTCACTCC 113
 QY 61 TCGACCCCGCTGCGGGCTAGTCCACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
 DB 114 TCGACCCCGCTGCGGGCTAGTCCACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 173
 QY 121 CCGCGCATGAGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
 DB 174 CCGCGCATGAGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 233
 QY 181 GCGCGCGGCGTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 240
 DB 234 GCGCGCGGCGTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 293
 QY 241 ACTGTGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTCCAGCTACCCCGGAGCT 300
 DB 294 ACTGTGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTCCAGCTACCCCGGAGCT 353
 QY 301 TTGATCCCTTACAGATGTGACCTATCAATGAA- GAGGACATCCTCTCCATGTTCTCAGC 359
 DB 354 TTGATCCCTTACAGATGTGACCTATCAATGAA- GAGGACATCCTCTCCATGTTCTCAGC 413

QY 360 TATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTGGCCCGGCC 419
 DB 414 TATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTGGCCCGGCC 473
 QY 420 TGACACCCCTGCTCTCAGGCGAGCACCAGTGGTTGGAAGGACATGTTCAATGTGAACGTGCT 479
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 QY 480 GGCCCTCAGCATCTGCACACGGGAAGCTTACCAGTCCATGAAGGAGCGGAATGTGGACGA 539
 DB 534 GGCCCTCAGCATCTGCACACGGGAAGCTTACCAGTCCATGAAGGAGCGGAATGTGGACGA 593
 QY 540 TGGGCACA-TCATTAAACATCAATAGCATGTCTGGCCACCGAGTGTACCC- TGTCTGTG 597
 DB 594 TGGGCACATTCATTAAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTG 653
 QY 598 ACCCACTTCTATAGTGGCCACCAAGTATGCCCTACTGCGCTGACAGAGGAGTACGAGC 655
 DB 654 AACCAATTCATAGTGGCCACCAAGTATGCCCTACTGCGCTGACAGAGGAGTACGAGC 711
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 DEFINITION 602297547F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4392011 5',
 mRNA sequence.
 ACCESSION BG030249
 VERSION BG030249.1 GI:12419347
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 932)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M10083 row: n column: 12
 High quality sequence stop: 601.
 Location/Qualifiers
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 /organism="Homo sapiens"
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 /note="Organ: Breast; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.383 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."
 ORIGIN
 Query Match 40.9%; Score 615.6; DB 10; Length 932;
 Best Local Similarity 94.7%; Pred. No. 9.5e-99;
 Matches 658; Conservative 0; Mismatches 35; Indels 2; Gaps 2;
 QY 264 GGTGCTGTAATGTAAGTGCAGGCTACCCCGGAGCTTTGATCCCTTACAGATGTGACCT 323
 DB 10 GGTGCTGTAATGTAAGTGCAGGCTACCCCGGAGCTTTGATCCCTTACAGATGTGACCT 69


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324 ATCAATGAAGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCAGCGGTGT 383
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384 AGACATCTGCATCAACATGCTGGCTTGGCCCGGCTGACACCTCTCTCAGGCGAGC 443
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130 AGACATCTGCATCAACATGCTGGCTTGGCCCGGCTGACACCTCTCTCAGGCGAGC 189
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444 CAGTGGTGGAGGACATGTTCAATGTGAAGTGAAGTGGCTTGGCCCGGCTGACACCTCTCTCAGGCGAGC 503
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564 CATGCTTGGCCACCGAGTGTACCCCTGTCTGTGACCCCACTTCTATAGTGGCCACCAAGTA 623
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310 CATGCTTGGCCACCGAGTGTACCCCTGTCTGTGACCCCACTTCTATAGTGGCCACCAAGTA 369
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684 CCGAGCCACGTGCACTCTCCAGTGTGGTGAGACACAAATTCGCTTCAAACCTCCAGCA 743
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804 TGTGGCCGAGGCTGTTAFTACGTCTCAGCAGCCCGGAGGAGTCTGAGGAGTCTTCCCTCCCG 863
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924 ACCCTTATGCTTGCCTTCTGCTCTGAGTCTTGAATTTA 958
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RESULT 22
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DEFINITION 60141804F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846168 5',
mRNA sequence.
BB617298
VERSION BE617298.1 GI:9888236
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-i@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 698.
Location/Qualifiers

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/clone_lib="NIH_MGC_65"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
ORIGIN
Query Match 40.1%; Score 603.4; DB 10; Length 923;
Best Local Similarity 99.8%; Pred. No. 1.4e-96;
Matches 604; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 332 AAGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCAGACGCGGTGTAGACATCT 391
Db 1 AAGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCAGACGCGGTGTAGACATCT 60
QY 392 GCATCAACAATGCTGGCTTGGCCCGGCTGACACCTCTCTCAGGAGCAGCCAGTGTGT 451
Db 61 GCATCAACAATGCTGGCTTGGCCCGGCTGACACCTCTCTCAGGAGCAGCCAGTGTGT 120
QY 452 GGAAGGACATGTTCAATGTGAACGTGTGGCCCTCAGCATCTGCACACGCGGAGCCTACC 511
Db 121 GGAAGGACATGTTCAATGTGAACGTGTGGCCCTCAGCATCTGCACACGCGGAGCCTACC 180
QY 512 AGTCCATGAGGAGCGGAATGTGACCATGGGACATCAATTAACATCAATAGCATGTCTG 571
Db 181 AGTCCATGAGGAGCGGAATGTGACCATGGGACATCAATTAACATCAATAGCATGTCTG 240
QY 572 GCCACCGAGTGTACCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCA 631
Db 241 GCCACCGAGTGTACCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCA 300
QY 632 CTGCGCTGACAGAGGAGTCTGAGCAAGAGTCTGGGAGGCGCCAGACCCACATCCGAGCCA 691
Db 301 CTGCGCTGACAGAGGAGTCTGAGCAAGAGTCTGGGAGGCGCCAGACCCACATCCGAGCCA 360
QY 692 CGTGCATCTCTCCAGGTTGGTGAGACAAATTCGCTTCAAACCTCCAGCAAGGAGC 751
Db 361 CGTGCATCTCTCCAGGTTGGTGAGACAAATTCGCTTCAAACCTCCAGCAAGGAGC 420
QY 752 CTGAGAGGAGGAGTCTGACCATCTATGAGCAATGAAGTGTCTCAAACCGAGGATGTGCCG 811
Db 421 CTGAGAGGAGGAGTCTGACCATCTATGAGCAATGAAGTGTCTCAAACCGAGGATGTGCCG 480
QY 812 AGGCTGTTATCTAGTCTCTCAGCAGCCCGGACACATCCAGATTCAGAGATCCAGATGA 871
Db 481 AGGCTGTTATCTAGTCTCTCAGCAGCCCGGACACATCCAGATTCAGAGATCCAGATGA 540
QY 872 GGCCTGAGGAGGAGTCTGAGTGTGAGGAGTCTGAGGAGTCTTCCCTCCCGACCTTCA 931
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QY 932 TGGCT 936
Db 601 TGGTT 605

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RESULT 23
LOCUS BM764342
DEFINITION K-EST0045842 SISNU5 Homo sapiens cDNA clone SISNU5-39-A06 5', mRNA
sequence.
ACCESSION BM764342
VERSION BM764342.1 GI:19093957
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 602)

REFERENCE
AUTHORS
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

TITLE
JOURNAL
COMMENT
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boseun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 39 row: A column: 06

High quality sequence stop: 602.

FEATURES
source

Location/Qualifiers
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/cell_type="Lymphoblast-like"

/cell_line="SNU-5"

/lab_host="Top10F"

/clone_lib="SISNUS"

/note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI;

Site 2: NciI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method.

The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 40.0%; Score 602; DB 12; Length 602;
Best Local Similarity 100.0%; Pred. No. 2.5e-96;
Matches 602; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 TGTCTCAGCTATCGGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGTGGCT 409
DB 1 TGTCTCAGCTATCGGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGTGGCT 60
QY 410 TGGCCCGGCTGACACCCCTGCTCTCAGGAGCAGCAGTGTGGAGGACATGTTCAATG 469
DB 61 TGGCCCGGCTGACACCCCTGCTCTCAGGAGCAGCAGTGTGGAGGACATGTTCAATG 120
QY 470 TGAAGCTGTGGCCCTCAGCATCTGCACACGGGAGCCCTACAGTCCATGAAGAGCGGA 529
DB 121 TGAAGCTGTGGCCCTCAGCATCTGCACACGGGAGCCCTACAGTCCATGAAGAGCGGA 180
QY 530 ATGTGGACATGGGACATCATTAATAGATGTCCTGGCCACCGAGTGTACCCC 589
DB 181 ATGTGGACATGGGACATCATTAATAGATGTCCTGGCCACCGAGTGTACCCC 240
QY 590 TGTCTGTGACCCACTTATAGTGCACCAAGTATGCCGTCTACTGGCTGACAGGGAC 649
DB 241 TGTCTGTGACCCACTTATAGTGCACCAAGTATGCCGTCTACTGGCTGACAGGGAC 300
QY 650 TGAGGCAAGAGCTTCGGGAGGCGCCAGACCCACATCCGAGCCACGTGTCATCTCTCCAGGTG 709

Db 301 TGAGGCAAGAGCTTCGGGAGGCGCCAGACCCACATCCGAGCCACGTGTCATCTCTCCAGGTG 360
QY 710 TGGTGGAGACAAATTCGCTTCAAATCTCAGCAAGGACCCCTGAGAAGCAGCTGCCA 769
Db 361 TGGTGGAGACAAATTCGCTTCAAATCTCAGCAAGGACCCCTGAGAAGCAGCTGCCA 420
QY 770 CCTATGAGCAAAATGAAGTGTCTCAAACCCGAGGATGTGGCGAGGCTGTATCTACGTCC 829
Db 421 CCTATGAGCAAAATGAAGTGTCTCAAACCCGAGGATGTGGCGAGGCTGTATCTACGTCC 480
QY 830 TCAGCACCCCGCACACATCCAGATTCGAGACATCCAGATGAGCCCAACGAGCAGGTGA 889
Db 481 TCAGCACCCCGCACACATCCAGATTCGAGACATCCAGATGAGCCCAACGAGCAGGTGA 540
QY 890 CCTAGTGACTGTGGAGCTCTCTCTCCCTCCACCCCTTCATGGCTTGCCTCTGCTC 949
Db 541 CCTAGTGACTGTGGAGCTCTCTCTCCCTCCACCCCTTCATGGCTTGCCTCTGCTC 600
QY 950 TG 951
Db 601 TG 602

RESULT 24

BI765897

LOCUS

DEFINITION

603046146F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186459 5',

mRNA sequence.

ACCESSION

BI765897

VERSION

BI765897.1 GI:15757475

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished (1999)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Inyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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High quality sequence stop: 748.

Location/Qualifiers

1..804

/organism="Homo sapiens"

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/clone="IMAGE:5186459"

/lab_host="DH10B"

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/note="Organ: pooled colon, kidney, stomach; Vector:

pcMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA

source anonymous pool of 3 colons, age 26 yo male, 49 yo

female, 71 yo male colon; 46 yo male kidney, and pool of 2

stomachs, 62 yo male and 70 yo female. Library is

oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.4 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 39.9%; Score 600.8; DB 12; Length 804;
Best Local Similarity 94.2%; Pred. No. 4e-96;

Matches	680;	Conservative	0;	Mismatches	32;	Indels	10;	Gaps	5;
QY	1	CGCGATCGACACCAAGCAGGTGCGCGCGCGCGCAGGAGCGCGCGCGCGCTCAGCTCC	60						
Db	83	CGCGATCGACACCAAGCAGGTGCGCGCGCGCGCAGGAGCGCGCGCGCTCAGCTCC	142						
QY	61	TCGACCCCGTGTCCGCGTGTAGTCCAGCGAGCGGACGGCGCGCTGGGCCCATGGCCAGG	120						
Db	143	TCGACTCCCGTGTCCGCGTGTAGTCCAGCGAGCGGACGGCGCGCTGGGCCCATGGCCAGG	202						
QY	121	CCCGCATGGAGGTGGCGACCGCGTGGTGCAGCGGGGCTTCGGGGGCGCATC	180						
Db	203	CCCGCATGGAGGTGGCGACCGCGTGGTGCAGCGGGGCTTCGGGGGCGCATC	262						
QY	181	GGCGCGCGCTGGCGCGCGCTGGTCCAGCAGGAGCTCAAGGTGGTGGCTGGCGCGC	240						
Db	263	GGCGCGCGCTGGCGCGCGCTGGTCCAGCAGGAGCTCAAGGTGGTGGCTGGCGCGC	322						
QY	241	ACTGTGGGCAACATCGAGGAGTGGCTGTGAATGTAAAGTGCAGGCTACCCCGGACT	300						
Db	323	ACTGTGGGCAACATCGAGGAGTGGCTGTGAATGTAAAGTGCAGGCTACCCCGGACT	382						
QY	301	TGATCCCGTTCAGATGTACCTATCAATGAAGAGGACATCTCTCCATGTCTCAGCT	360						
Db	383	TGATCCCGTTCAGATGTACCTATCAATGAAGAGGACATCTCTCCATGTCTCAGCT	442						
QY	361	ATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACATGCTGGCTGGCGCGCT	420						
Db	443	ATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACATGCTGGCTGGCGCGCT	502						
QY	421	GACACCTGTCTCAGGAGCAGCAGTGTGGAGGACATGTTCATATGTGAACGTGTG	480						
Db	503	GACACCTGTCTCAGGAGCAGCAGTGTGGAGGACATGTTCATATGTGAACGTGTG	562						
QY	481	GCCCTCAGCATCTGCACACGGAGCCTACAGTCCATGAAGAGCGGAATGTGG--ACG	538						
Db	563	GCCCTCAGCATCTGCACACGGAGCCTACAGTCCATGAAGAGCGGAATGTGGAAACG	622						
QY	539	ATGGGCAACATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCT-GTCTGTG	597						
Db	623	ATGGGCAACATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTG	682						
QY	598	ACCACTTCTATA--GTGCCACCAAGTATGCGTCACTGCGC--TGACAGAGGACTGA	652						
Db	683	ACCACTTCTATAAGTGCACCAAGTATGCGTCACTGCGC--TGACAGAGGACTGA	742						
QY	653	GGCAAGAG--CTTCGGAGGCGCCAGACCCACATCGAGCCACGTGTCATCTCCAGTGT	710						
Db	743	GGCAAGAGCTTCGGGAAGGCGCAAAACCAACATCGAGACAAAGTGCATCTCTCAGTGT	802						
QY	711	GG 712							
Db	803	TG 804							
RESULT	25								
LOCUS	BU539642								
DEFINITION	AGENCOURT 10224058 NIH_MGC_107 Homo sapiens cDNA clone								
IMAGE	IMAGE:6570429 5', mRNA sequence.								
ACCESSION	BU539642								
VERSION	BU539642.1								
KEYWORDS	EST.								
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
TITLE	1 (bases 1 to 937)								
JOURNAL	NIH-MGC http://mgi.nci.nih.gov/								
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)								
	Unpublished (1999)								
	Contact: Robert Strausberg, Ph.D.								
	Email: cgapbs-rc@mail.nih.gov								

Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2759 row: e column: 21
 High quality sequence stop: 527.

FEATURES
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 /clone="IMAGE:6570429"
 /tissue_type="adenocarcinoma, cell_line"
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 /clone_lib="NIH_MGC_107"
 /note="Organ: breast; Vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 39.6%; Score 596.6; DB 13; Length 937;
 Best Local Similarity 95.4%; Pred. No. 2.2e-95;
 Matches 625; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

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QY	195	CCGGGCGCTGTCCAGCAGGAGCTGAAGTGGTGGGTGGCGCGCGCTGCTGGGCAACAT	254
Db	61	CCGGGCGCTGTCCAGCAGGAGCTGAAGTGGTGGGTGGCGCGCGCTGCTGGGCAACAT	120
QY	255	CGAGGAGTGGCTCTGAATGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	314
Db	121	CGAGGAGTGGCTCTGAATGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	180
QY	315	ATGTGACCTATCAATGAAGAGGACATCTCTCCATGTCTCAGCTATCCGTTCTCAGCA	374
Db	181	ATGTGACCTATCAATGAAGAGGACATCTCTCCATGTCTCAGCTATCCGTTCTCAGCA	240
QY	375	CAGCGGTGTAGACATCTGCATCAACATGTGGTGGCGCGCGCTGACACCCCTGCTC	434
Db	241	CAGCGGTGTAGACATCTGCATCAACATGTGGTGGCGCGCGCTGACACCCCTGCTC	300
QY	435	AGGCGACACAGTGGTGGAGGAGCATGTTCAATGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	494
Db	301	AGGCGACACAGTGGTGGAGGAGCATGTTCAATGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	360
QY	495	CACACGGAGGAGCTACCCAGTCCATGAAGAGGAGCGGAATGTGGAGTGGGCGACATCATTA	554
Db	361	CACACGGAGGAGCTACCCAGTCCATGAAGAGGAGCGGAATGTGGAGTGGGCGACATCATTA	420
QY	555	CATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACACCCCTTCTATAGTGC	614
Db	421	CATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACACCCCTTCTATAGTGC	480
QY	615	CACCAAGTATGCGCTCACTGCGCTGACAGAGGAGCTGAGGCAAGAGCTTCGGAGGAGCCCA	674
Db	481	CACCAAGTATGCGCTCACTGCGCTGACAGAGGAGCTGAGGCAAGAGCTTCGGAGGAGCCCA	540
QY	675	GACCCACATCCGAGGAGCCGCTGCTCTCAGGTGGTGGGAGACAAATT-CGCGCTTCA	733
Db	541	GACCCACATCCGAGGAGCCGCTGCTCTCAGGTGGTGGGAGACAAATT-CGCGCTTCC	600
QY	734	AACTCCACAGACAGGAGCCCTGAGAGGAGCTGCCACCTATGAGCAAAATGAAGT	788

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Db 601 AACTCCAGAACAGGACCCCTTGAGAAAGGCTTCTGCCACCTATGAACCAATG 655
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BM793929 691 bp mRNA linear EST 05-MAR-2002
LOCUS K-EST0074920 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-32-C08
DEFINITION 5', mRNA sequence.
ACCESSION BM793929
VERSION BM793929.1 GI:19142161
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 691)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 32 row: C column: 08
High quality sequence stop: 691.
Location/Qualifiers
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/sex="F"
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/cell_type="Lymphoblast-like"
/lab_host="SNU-16"
/clone_lib="S22SNU16n1"
/note="Organ: Stomach; Vector: pT73-Pac; Site: 1: EcoRT;
Site 2: NotI; The S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldi, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6 (9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."
ORIGIN
Query Match 39.0%; Score 586.4; DB 12; Length 691;
Best Local Similarity 88.0%; Pred. No. 1.4e-93;
Matches 690; Conservative 0; Mismatches 1; Indels 93; Gaps 1;
QY 472 AAGCTGCTGGCCCTCAGCATCTGCACACGGGAAGCCCTACGATCCATGAAGGAGCGGAAT 531
Db 1 AAGCTGCTGGCCCTCAGCATCTGCACACGGGAAGCCCTACGATCCATGAAGGAGCGGAAT 60
QY 532 GTGACGATGGGCACATCATTAACATCATATAGATGTCTGGCCACCGAGTGTACCCCTG 591
Db 61 GTGACGATGGGCACATCATTAACATCATATAGATGTCTGGCCACCGAGTGTACCCCTG 120
QY 592 TCTGTGACCCACTTCTATAGTGGCCACCAAGTATGCGGTCACTCGCTGCAGAGGAGACTG 651
Db 121 TCTGTGACCCACTTCTATAGTGGCCACCAAGTATGCGGTCACTCGCTGCAGAGGAGACTG 180
QY 652 AGGCAAGAGCTTCGGGAGGGCCAGACCCACATCCGAGCCACGTGTCATCTCTCCAGGTGTG 711
Db 181 AGGCAAGAGCTTCGGGAGGGCCAGACCCACATCCGAGCCAC----- 221

RESULT 26
BM793929
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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/sex="F"
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/lab_host="SNU-16"
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/note="Organ: Stomach; Vector: pT73-Pac; Site: 1: EcoRT;
Site 2: NotI; The S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldi, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6 (9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."

QY 712 GTGGAGACACAATTTCGCTTCAAACTCCACGACAAGAGCCCTGAGAGGACGCTGCCACC 771
Db 222 ----- 221
QY 772 TATGAGCAATGAAGTGTCTCAAAACCCGAGGATGTGCCGAGGCTGTATCTACGTCTC 831
Db 222 -----GTGTCTCAAAACCCGAGGATGTGCCGAGGCTGTATCTACGTCTC 267
QY 832 AGCACCCCGCACATCCAGATTGGAGATCCAGATGAGGCCACGAGCAGGTGACC 891
Db 268 AGCACCCCGCACATCCAGATTGGAGATCCAGATGAGGCCACGAGCAGGTGACC 327
QY 892 TAGTGACTGTGGGAGCTCTCTCTCCCTCCCAACCTTTCATGGCTTGCTCTCGCTCTG 951
Db 328 TAGTGACTGTGGGAGCTCTCTCTCCCTCCCAACCTTTCATGGCTTGCTCTCGCTCTG 387
QY 952 GATTTTAGTGTGTTGATTTCTGGATCAGGGGATACCACTTCTCTCCACACCCGACGAGG 1011
Db 388 GATTTTAGTGTGTTGATTTCTGGATCAGGGGATACCACTTCTCTCCACACCCGACGAGG 447
QY 1012 GGCTAGAAAAATTTGTTGAGATTTTATATCATCTGTCAAAATGCTTCAGTTGTAATG 1071
Db 448 GGCTAGAAAAATTTGTTGAGATTTTATATCATCTGTCAAAATGCTTCAGTTGTAATG 507
QY 1072 TGAATAATGGCTCGGGAAAGAGGTGTGTCCCTAAATGTTTAACTTGTTC 1131
Db 508 TGAATAATGGCTCGGGAAAGAGGTGTGTCCCTAAATGTTTAACTTGTTC 567
QY 1132 TTGTGCCCTCGGCACATTGGCTTTGTCTGTCTCAGTGTCTTCCCTTTGACATGGGAAA 1191
Db 568 TTGTGCCCTCGGCACATTGGCTTTGTCTGTCTCAGTGTCTTCCCTTTGACATGGGAAA 627
QY 1192 GGAGTTGTGGCCAAAATCCCATCTTCTTGACACCTCAACGCTGTGGCTCAGGGCTGGGG 1251
Db 628 GGAGTTGTGGCCAAAATCCCATCTTCTTGACACCTCAACGCTGTGGCTCAGGGCTGGGG 687
QY 1252 TGGC 1255
Db 688 TGGC 691

RESULT 27
AL559036 1022 bp mRNA linear EST 31-MAY-2003
LOCUS AL559036 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
DEFINITION Homo sapiens cDNA clone CS0DJ010YN13 5-PRIME, mRNA sequence.
ACCESSION AL559036
VERSION AL559036.2 GI:31283169
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 1022)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12904138.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8845.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DJ010CG07QP1&cluster=8845.f. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DJ010CG07QP1.
FEATURES
Location/Qualifiers
1..1022
source
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/clone="CS007010Y13"
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/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized"

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ORIGIN

Query Match	38.9%;	Score 586;	DB 9;	Length 1022;
Best Local Similarity	100.0%;	Prod. No. 1.6e-93;		
Matches 586;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	920	CCCCACCCCTCATGGCTTGCCTCTGCCTCTGGATTTTAGTGTTGATTTCTTGGATCAGC	979	
Db	367	CCCCACCCCTCATGGCTTGCCTCTGCCTCTGGATTTTAGTGTTGATTTCTTGGATCAGC	426	
QY	980	GGATACCACTTCTGTGCCACACCCCGACAGGGGCTAGAAAATTGTGTTTCAGATTTTTAT	1039	
Db	427	GGATACCACTTCTGTGCCACACCCCGACAGGGGCTAGAAAATTGTGTTTCAGATTTTTAT	486	
QY	1040	ATCATCTTCTCAAAATGCTTCAGTTGTAATGTGAAAATGGGCTGGGGAAGAGGTGG	1099	
Db	487	ATCATCTTGTCAAAATGCTTCAGTTGTAATGTGAAAATGGGCTGGGGAAGAGGTGG	546	
QY	1100	TGTCCTTAATTTGTTTACTTGTGTAACCTTGTCTTGTGCCCTCGGGCACTTGGCCTTTGTC	1159	
Db	547	TGTCCTTAATTTGTTTACTTGTGTAACCTTGTCTTGTGCCCTCGGGCACTTGGCCTTTGTC	606	
QY	1160	TGCTCTCAGTGCTTCCCTTTTGACATGGGAAAGAGTGTGGCCAAAATCCCCATCTTCT	1219	
Db	607	TGCTCTCAGTGCTTCCCTTTTGACATGGGAAAGAGTGTGGCCAAAATCCCCATCTTCT	666	
QY	1220	TGCACCTCAACGTCCTGTGCTCAGGGCTGGGGTGGCAGAGGGAGGCTTCACCTTATATC	1279	
Db	667	TGCACCTCAACGTCCTGTGCTCAGGGCTGGGGTGGCAGAGGGAGGCTTCACCTTATATC	726	
QY	1280	TGTGTTGTTATCAGGGCTCCAGACTTCTCTCTGCTGCCCCACTGCACCCCTCTCCCC	1339	
Db	727	TGTGTTGTTATCCAGGGCTCCAGACTTCTCTCTGCTGCCCCACTGCACCCCTCTCCCC	786	
QY	1340	CTTATCTATCTCTCTCTGGCTCCCCAGCCGAGTCTTGGCTTCTTGTCCCTCTCTGGGGT	1399	
Db	787	CTTATCTATCTCTCTCTGGCTCCCCAGCCGAGTCTTGGCTTCTTGTCCCTCTCTGGGGT	846	
QY	1400	CATCCCTCCACTCTGACTCTGACTATGGCAGCAGAAACACAGGGCTGCCCACGTGGATT	1459	
Db	847	CATCCCTCCACTCTGACTCTGACTATGGCAGCAGAAACACAGGGCTGCCCACGTGGATT	906	
QY	1460	TCATGGTGATCATTTAAAAAGAAAAATCGCAACCAAAAAA	1505	
Db	907	TCATGGTGATCATTTAAAAAGAAAAATCGCAACCAAAAAA	952	

RESULT 28

BM737591	582 bp	mRNA	linear	EST 01-MAR-2002
LOCUS				
DEFINITION	K-EST0000094	SiSNUS Homo sapiens cDNA clone	SiSNUS-21-B02 5', mRNA	
ACCESION	sequence.			
VERSION	BM737591.1	GI:19058920		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 582)			
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,			

Oh, K. J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and Kim, Y. S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel : +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 21. row: B column: 02
High quality sequence stop: 582.

FEATURES

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/clone_lib="S15NU5"

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/note=Organ: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library "

ORIGIN

Query Match	38.6%	Score 580.4	DB 12	Length 582
Best Local Similarity	99.8%	Pred. No. 1.6e-92		
Matches 581	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	365	GTCTCAGCACGGGTGTAGACATCTGCATCAACAATGCTTGGCCGGCTGACA	424	
Db	1	GTCTCAGCACGGGTGTAGACATCTGCATCAACAATGCTTGGCCGGCTGACA	60	
QY	425	CCCTGCTCTCAGGCAGCACACAGTGGTTGGGAAGGACATGTTCAATGTGTAAGCTGTGCGCC	484	
Db	61	CCCTGCTCTCAGGCAGCACACAGTGGTTGGGAAGGACATGTTCAATGTGTAAGCTGTGCGCC	120	
QY	485	TCAGCATCTGCACACGGGAAGCCTACAGTCCATGAAGAGCGGAATGTGCAGATGGGC	544	
Db	121	TCAGCATCTGCACACGGGAAGCCTACAGTCCATGAAGAGCGGAATGTGCAGATGGGC	180	
QY	545	ACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACCCACT	604	
Db	181	ACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACCCACT	240	
QY	605	TCATATAGTCCCAACCAAGTATCGCGTCACTCGCGTGCAGAGGACTGAGCAAGACTTC	664	
Db	241	TCATATAGTCCCAACCAAGTATCGCGTCACTCGCGTGCAGAGGACTGAGCAAGACTTC	300	
QY	665	GGGAGGCCAGACCCACATCCGAGGCCACGTGCAATCTCCAGTGTGGTGGAGACACAAT	724	
Db	301	GGGAGGCCAGACCCACATCCGAGGCCACGTGCAATCTCCAGTGTGGTGGAGACACAAT	360	
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Db      361 TCGCCTTCAAACTCCACGACAGACCCCTGAGAAGGAGCGTCCACCATATGAGCAATGA 420
Qy      785 AGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTATTACTAGTCTCAGCACCCCGCCAC 844
Db      421 AGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTATTACTAGTCTCAGCACCCCGCCAC 480
Qy      845 ACATCCAGATGGAGACATCCAGATGAGGCCCGACGAGCAGGTGACCTAGTACTGTGGG 904
Db      481 ACATCCAGATGGAGACATCCAGATGAGGCCCGACGAGCAGGTGACCTAGTACTGTGGG 540
Qy      905 AGCTCCCTCCCTCCCTCCCGCCCTTCATGGCTTCCTCCCTCCG 946
Db      541 AGCTCCCTCCCTCCCTCCCGCCCTTCATGGCTTCCTCCCTCCG 582

RESULT 29
LOCUS   BE386240
DEFINITION 601273447F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614770 5',
mRNA sequence.
ACCESSION BE386240
VERSION BE386240.1 GI:9331605
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM277 row: m column: 11
High quality sequence stop: 652.
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/clone="IMAGE:3614770"
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/clone_lib="NIH_MGC_20"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGACAGG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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ORIGIN

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Query Match 38.4%; Score 578.4; DB 10; Length 769;
Best Local Similarity 94.6%; Pred. No. 3.6e-92;
Matches 643; Conservative 0; Mismatches 31; Indels 6; Gaps 4;

Qy      800 AGGATGTGGCCGAGGCTGTATTACGTCTCAGCACCCCGCACATCCAGATTGGAG 859
Db      1 AGGATGTGGCCGAGGCTGTATTACGTCTCAGCACCCCGCACATCCAGATTGGAG 60
Qy      860 ACATCCAGATGAGGCCCGACGAGCAGGTGACCTAGTACTGTGGGAGCTCCCTCCCT 919
Db      61 ACATCCAGATGAGGCCCGACGAGCAGGTGACCTAGTACTGTGGGAGCTCCCTCCCT 120
Qy      920 CCCACCCCTTCATGGCTTGCCCTCCTGCCTCTGGATTTTAGGTGTTGATTTCTGGATCAGC 979
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Db      121 CCCACCCCTTCATGGCTTGCCCTCCTGCCTCTCGATTTTAGGTGTTGATTTCTGGATCAGC 180
Qy      980 GGATACCACTTCTGTCTCCACACCCCGACGAGGCTAGAAAATTTGTTTCAGATTTTAT 1039
Db      181 GGATACCACTTCTGTCTCCACACCCCGACGAGGCTAGAAAATTTGTTTCAGATTTTAT 240
Qy      1040 ATCATCTTGTCAAAATGCTTTCAGTTGTAATTTGTAATAATGGGCTGGGAAAGAGGTGG 1099
Db      241 ATCATCTTGTCAAAATGCTTTCAGTTGTAATTTGTAATAATGGGCTGGGAAAGAGGTGG 300
Qy      1100 TGTCCCTAAATTTGTTTAACTTTAACTTTGTTGTCCTCCCTGGGCACTTGGCCCTTTGTC 1159
Db      301 TGTCCCTAAATTTGTTTAACTTTAACTTTGTTGTCCTCCCTGGGCACTTGGCCCTTTGTC 360
Qy      1160 TGTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGGTGTTGGCCAAAATCCCAATCTTCT 1219
Db      361 TGTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGGTGTTGGCCAAAATCCCAATCTTCT 420
Qy      1220 TGACCTTCAACGCTCTGTGGCTCAGGGCTGGGGTGGCAGAGGAGGCTTCACTTATATC 1279
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Qy      1280 TGTCTTGTATCCAGGCTCCAGACTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1339
Db      481 TGTCTTGTATCCCA-GGCTCCAGACTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 537
Qy      1340 CTTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1399
Db      538 CTTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 595
Qy      1400 CATCCCTCCACTCTGACTCTGACTA-TGGCAGCAGAACACACAGGGGCTGGGCCAGTGGAT 1458
Db      596 CATCCCTCCACTCTGACTCTGACTA-TGGCAGCAGAACACACAGGGGCTGGGCCAGTGGAT 655
Qy      1459 TTCATGGTGCATCTTAAAAA 1478
Db      656 TCTGTGATCTTTAAAGAAA 675
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RESULT 30

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LOCUS   BM742038
DEFINITION K-EST0014773 S1SNU5s1 Homo sapiens cDNA clone S1SNU5s1-1-B09 5',
mRNA sequence.
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ACCESSION BM742038

VERSION BM742038.1 GI:19063367

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 573)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

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High quality sequence stop: 573.

Location/Qualifiers

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/notes="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
with tabacco acid pyrophosphatase (TAP). The deapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and
sequencing about 2,000 ~ 3,000 colonies in original cDNA
library, the abundant cDNAs were selected and amplified by
PCR reaction using vector region primer including T7
promotor as 5' primer and N(dT)14 as 3' primer. The PCR
products were used as template for synthesis of
biotinylated single stranded RNA by in vitro transcription
reaction. The synthesized RNA probes were hybridized with
antisense single stranded cDNAs prepared from original
library and incubated with avidin-gel. After removing
DNA-RNA hybrids by centrifuge, the subtraced cDNA
libraries were constructed by transformation of the
remaining DNA into competent cells E. coli Top10F with
electroporation method."

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ORIGIN

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Query Match      38.1%; Score 573; DB 12; Length 573;
Best Local Similarity 100.0%; Pred. No. 3.3e-91;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 TGTCTCAGCTATCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATCTGGCT 409
DB 1 TGTCTCAGCTATCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATCTGGCT 60
QY 410 TGGCCCGGCTGACACCTGCTCTCAGGACGACAGTGGTGAAGACATGTTAATG 469
DB 61 TGGCCCGGCTGACACCTGCTCTCAGGACGACAGTGGTGAAGACATGTTAATG 120
QY 470 TGAACGTGCTGGCCCTCAGCATCTGCACAGGGAAGCTTACCAGTCCATGAAGGAGCGGA 529
DB 121 TGAACGTGCTGGCCCTCAGCATCTGCACAGGGAAGCTTACCAGTCCATGAAGGAGCGGA 180
QY 530 ATGTGACGATGGGCATCATTTAACTAATAGCATGTGTGGCCACCGAGTGTATCCCC 589
DB 181 ATGTGACGATGGGCATCATTTAACTAATAGCATGTGTGGCCACCGAGTGTATCCCC 240
QY 590 TGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCATCTGCCTCAGAGAGGAC 649
DB 241 TGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCATCTGCCTCAGAGAGGAC 300
QY 650 TGAGGCAAGAGCTTCGGGAGGCGCCAGACCCACATCCGAGCCAGTGTGCATCTCTCCAGGTG 709
DB 301 TGAGGCAAGAGCTTCGGGAGGCGCCAGACCCACATCCGAGCCAGTGTGCATCTCTCCAGGTG 360
QY 710 TGTGTGAGACACAATTCGCTTCAAACTCCAGCAAGGACCCCTGAGAGGCGAGCTGCCA 769
DB 361 TGTGTGAGACACAATTCGCTTCAAACTCCAGCAAGGACCCCTGAGAGGCGAGCTGCCA 420
QY 770 CCTATGAGCAAAATGAAATGTCTCAAAACCCAGAGATGTGGCCGAGGCTGTATCTACGTCC 829
DB 421 CCTATGAGCAAAATGAAATGTCTCAAAACCCAGAGATGTGGCCGAGGCTGTATCTACGTCC 480

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QY 830 TCAGCACCCCCCACCACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCAGGTGA 889
DB 481 TCAGCACCCCCCACCACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCAGGTGA 540
QY 890 CCTACTGACTGTGGGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 922
DB 541 CCTACTGACTGTGGGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 573

RESULT 31
BE869917
LOCUS BE869917
DEFINITION BE869917
ACCESSION BE869917
VERSION BE869917.1 GI:10318693
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 614)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9569 row: n column: 15
High quality sequence stop: 602.

FEATURES
source
location/Qualifiers
1..614
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3850574"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match      37.7%; Score 567.4; DB 10; Length 614;
Best Local Similarity 99.2%; Pred. No. 3.2e-90;
Matches 612; Conservative 0; Mismatches 1; Indels 4; Gaps 4;

QY 33 GGACGAGAGCGCCCGGGCTCAGCTCTCTCGACCCCGCTGTTCGGGCTAGTCCAGCGAGGC 92
DB 1 GGACGAGAGCGCCCGGGCTCAGCTCTCTCGACCCCGCTGTTCGGGCTAGTCCAGCGAGGC 60
QY 93 GGACGAGCGCGCTGGGCGCCATGCGCCAGGCCCGCGATGGCGCGGTGGCGCGCGGTGGC 152
DB 61 GGACGAGCGCGCTGGGCGCCATGCGCCAGGCCCGCGATGGCGCGGTGGCGCGCGGTGGC 120
QY 153 GTTGTGTGACGGGGGCTCGGGGGGCTCGGGGGGCTCGGGGGGCTCGGGGGGCTCGGGGGG 212
DB 121 GTTGTGTGACGGGGGCTCGGGGGGCTCGGGGGGCTCGGGGGGCTCGGGGGGCTCGGGGG 179
QY 213 GGGACTGAAGGTGGTGGGCTGCGCCGCACTGTGGGCAACATCGAGGAGCTGGCTCTCA 272
DB 180 GGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCGAGGAGCTGGCTCTCA 239
QY 273 ATGTAAAGTGTGAGGCTACCCCGGAGCTTTGATCCCTACAGATGTACATCAATAACA 332

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Db 240 ATGTAGAGTGCAGGCTACCCGGGACTTTGATCCCTCAGATGTCACATATCAATGA 299
 QY 333 AGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACACCGGTGTAGACATCTG 392
 Db 300 AGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACACCGGTGTAGACATCTG 359
 QY 393 CATCAACAATGCTGGCTGGCCCGGCTGTGACACCTGCTCTCAGGACGACCACTGTTG 452
 Db 360 CATCAACAATGCTGGCTGGCCCGGCTGTGACACCTGCTCTCAGGACGACCACTGTTG 419
 QY 453 GAAGGACATGTTCAATGTGAAGCTGTGGCCCTCAGCATCTGCACACGGAAGCTTACCA 512
 Db 420 GAAGGACATGTTCAATGTGAAGCTGTGGCCCTCAGCATCTGCACACGGAAGCTTACCA 479
 QY 513 GTCCATGAAGAGCGGAATGTGGACGATGGGCAATCATTAACATCAATAGCATGTCTGG 572
 Db 480 GTCCATGAAGAGCGGAATGTGGACGATGGGCAATCATTAACATCAATAGCATGTCTGG 539
 QY 573 CCACGAGTGTACCCCTGTGTGACCCACTTCTATAGTCCACCAAGTATGCCGTAC 632
 Db 540 CCA-CGAGTGTACCCCTGTGTGACGCA-TTCTATAGTCCACCAAGTATG-CGTAC 596
 QY 633 TGCCTGCACAGGGAC 649
 Db 597 TGCCTGCACAGGGAC 613

RESULT 32
 BM744024
 LOCUS
 DEFINITION K-EST0017362 S1SNU5s1 Homo sapiens cDNA clone S1SNU5s1-4-C01 5',
 mRNA sequence.

ACCESSION
 VERSION
 BM744024.1 GI:19065353

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 566)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

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Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 4 row: C column: 01

High quality sequence stop: 566.

Location/Qualifiers

1..566

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S1SNU5s1-4-C01"

/sex="F"

/tissue_type="Ascites"

/cell_type="Lymphoblast-like"

/cell_line="SNU-5"

/lab_host="Top10F"

/clone_lib="S1SNU5s1"

/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by

priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library. After analyzing and
 sequencing about 2,000 ~ 3,000 colonies in original cDNA
 library, the abundant cDNAs were selected and amplified by
 PCR reaction using vector region primer including T7
 promoter as 5' primer and N(dt)14 as 3' primer. The PCR
 products were used as template for synthesis of
 biotinylated single stranded RNA by in vitro transcription
 reaction. The synthesized RNA probes were hybridized with
 antisense single stranded cDNAs prepared from original
 library and incubated with avidin-gel. After removing
 DNA-RNA hybrids by centrifuge, the subtracted cDNA
 libraries were constructed by transfection of the
 remaining DNA into competent cells E. coli Top10F with
 electroporation method."

ORIGIN

Query Match 37.6%; Score 566; DB 12; Length 566;
 Best Local Similarity 100.0%; Pred. No. 5.7e-90;
 Matches 566; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 TGTTCCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACATGCTGGCT 409
 Db 1 TGTTCCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACATGCTGGCT 60

QY 410 TGGCCCGGCTGTGACACCTGCTCTCAGGACACACAGTGGTTGAAGACATGTTCAATG 469
 Db 61 TGGCCCGGCTGTGACACCTGCTCTCAGGACACACAGTGGTTGAAGACATGTTCAATG 120

QY 470 TGAACGCTGTGCGCCCTCAGCATCTGCACACGGGAGCCTACAGTCCATGAAGAGCGGA 529
 Db 121 TGAACGCTGTGCGCCCTCAGCATCTGCACACGGGAGCCTACAGTCCATGAAGAGCGGA 180

QY 530 ATGTGGACGATGGGACATCATTAACATCATAGCATGTCTGGCCACCGAGTGTACCCC 589
 Db 181 ATGTGGACGATGGGACATCATTAACATCATAGCATGTCTGGCCACCGAGTGTACCCC 240

QY 590 TGTCTGTGACCCACTTCTATAGTGCACCAAGTATGCCGTCACTCGCTGACAGAGGAC 649
 Db 241 TGTCTGTGACCCACTTCTATAGTGCACCAAGTATGCCGTCACTCGCTGACAGAGGAC 300

QY 650 TGAGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCACGTCATCTCTCCAGGTG 709
 Db 301 TGAGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCACGTCATCTCTCCAGGTG 360

QY 710 TGGTGGACACAAATTCGCTTCAACCTCCAGCACAGGACCCCTGAGAAGCGAGCTGCCA 769
 Db 361 TGGTGGACACAAATTCGCTTCAACCTCCAGCACAGGACCCCTGAGAAGCGAGCTGCCA 420

QY 770 CCTATGAGCAATGAAGTGTCTCAAAACCGGAGGATGTGGCCGAGGCTGTATCTACGTC 829
 Db 421 CCTATGAGCAATGAAGTGTCTCAAAACCGGAGGATGTGGCCGAGGCTGTATCTACGTC 480

QY 830 TCAGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCGAGTGA 889
 Db 481 TCAGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCGAGTGA 540

QY 890 CCTAGTACTGTGGGAGCTCTCCCTT 915
 Db 541 CCTAGTACTGTGGGAGCTCTCCCTT 566

RESULT 33
 BM82228/c
 LOCUS
 DEFINITION UI-E-EJ0-aio-j-09-0-UI.s1 UI-E-EJ0 Homo sapiens cDNA clone

BM82228 572 bp mRNA linear EST 27-FEB-2002
 UI-E-EJ0-aio-j-09-0-UI.s1

UI-E-EJ0-ai0-j-09-0-UI 3', mRNA sequence.
 BM682228
 VERSION BM682228.1 GI:18992124
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 572)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
 The following repetitive elements were found in this cDNA sequence: 1-38, >POLY_A#Simple_repeat (matched complement)
 Seq primer: M13 Forward
 POLYA=yes.

FEATURES

source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="UI-E-EJ0"
 /tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
 /dev_stage="fetal and adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-E-EJ0"
 /note="Organ: eye; Vector: pT73-pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-EJ0 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGATCAAGG; lens, CGATTAGCGA; eye anterior segment, AATGCCGCGAT; optic nerve, CCATTAAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG TISSUE=human retina
 TAG LIB=UI-E-EJ0
 TAG_SEQ=CCGCG"

ORIGIN

Query Match 37.5%; Score 565; DB 12; Length 572;
 Best Local Similarity 99.8%; Pred. No. 8.6e-90;
 Matches 565; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 940 CTCCTGCGCTGGATTAGGTTTCTGGATCAGGGATACACTTCCTGTCAC 999
 DB 572 CTCCTGCGCTGGATTAGGTTTCTGGATCAGGGATACACTTCCTGTCAC 513

QY 1000 ACCCGACACAGGGCTAGAAAAATTTGTTGAGATTTTATATCATCTTGTCAAATGCTT 1059
 DB 512 ACCCGACACAGGGCTAGAAAAATTTGTTGAGATTTTATATCATCTTGTCAAATGCTT 453
 QY 1060 CAGTTGTAATGTGAATAATGGCTGGGAAAGGAGGTGCTCCCTAATGTTTACTT 1119
 DB 452 CAGTTGTAATGTGAATAATGGCTGGGAAAGGAGGTGCTCCCTAATGTTTACTT 393
 QY 1120 GTTAACTTGTCTTGTGCCCCCTGGGCACCTTGGCCCTTGTCTCTCAGTGTCTTCCCTT 1179
 DB 392 GTTAACTTGTCTTGTGCCCCCTGGGCACCTTGGCCCTTGTCTCTCAGTGTCTTCCCTT 333
 QY 1180 TGACATGGGAAAGGAGTTGTGGCCAAAATCCCACTTCTTTCACCTCAACGCTGTGGC 1239
 DB 332 TGACATGGGAAAGGAGTTGTGGCCAAAATCCCACTTCTTTCACCTCAACGCTGTGGC 273
 QY 1240 TCAGGGCTGGGCTGGCAGAGGAGGCTTCACTTATATCTGTGTGTTATCCAGGGCTC 1299
 DB 272 TCAGGGCTGGGCTGGCAGAGGAGGCTTCACTTATATCTGTGTGTTATCCAGGGCTC 213
 QY 1300 CAGACTTCTCTCTGCTGCCCCCTGCACCTGCACCCCTCTCCCTTATCTCTCTCTCGG 1359
 DB 212 CAGACTTCTCTCTGCTGCCCCCTGCACCTGCACCCCTCTCCCTTATCTCTCTCGG 153
 QY 1360 CTCGCCAGCCAGCTTGGCTTCTTGTCCTCCCTCTCGGGCTCATCCCTCCACTCTGACTCT 1419
 DB 152 CTCGCCAGCCAGCTTGGCTTCTTGTCCTCCCTCTCGGGCTCATCCCTCCACTCTGACTCT 93
 QY 1420 GACTATGCGCAGCAGAACACAGGGCTGGCCAGTGGATTTCATGGTGATCATTAATAAAA 1479
 DB 92 GACTATGCGCAGCAGAACACAGGGCTGGCCAGTGGATTTCATGGTGATCATTAATAAAA 33
 QY 1480 GAAAAATCGCAACCAAAAAA 1505
 DB 32 GAAAAATCGCAACCAAAAAA 7

RESULT 34
 BI761329
 LOCUS BI761329 748 bp mRNA linear EST 25-SEP-2001
 DEFINITION 603044093F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5184479 5', mRNA sequence.
 ACCESSION BI761329
 VERSION BI761329.1 GI:15752907
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 748)
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabs-i@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLAM1460 row: i column: 24
 High quality sequence stop: 724.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5184479"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_116"

FEATURES

source
 1. 748
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5184479"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_116"

10 GACGAAAGCACTCCGCCGGCGGCATGGAGAGCGGCCGGGGTCAGCTCCTCGACCCCC 69

70 GACCAAGCAGGTCTGGCGGCGGGCAGGAGAGCGGGCGGTCTCTCGACCCC 129

130 GTGTGGGCTAGTCCATGCGAGGCGTCACTGGGCTGGCGTGGTGCCTGTGCCAGGCC 189

[illegible]

180 CGGGCGGGCCGTGGCCC-GGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGGGCC 238

239 GCACTGTGGGCAACATCGAGGAGCTGGTCTCTGAATGTAAGAGTGCAGGCTACCCCGGGA 298

299 CTTTGATCCCCCTACAGATGTGACCTATCAAAATGAAGAGGACATCCTCTCCATGTTCTCAG 358

[illegible]

430 CTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTGGCCCGGC 489

490 CTGAACCCCTGCTCTCAGGCAGCACCACTGGTTGGAAGGACATGTTCAATGTGAACGTGC 549

550 TGGCCCTCAGCATCTTTGCAACGCGGAAGCCTACAGTCCATGAAGGAGCGGAATGTGGAC 609

[illegible]

597 GACCCACTTCTATAGTGGCCACCAAGTATGCCGCTCAGACAGGGACTGAGGCA 658

QY 657 AGAGCTTCGGG 667

[illegible]

ACCESSION	BG967186
VERSION	BG967186.1
	GI:14354823

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Db      539 GCACATCAATTAACATCAACAGCATGTGTGGCCACCGAGTCCACCCAGTCTGTGATCCA 598
QY      603 TTCTATAGTCCACCAAGTATCCCTCACTGCGCTGACAGAGGACTGAGGCAAGACT 662
Db      599 TTCTATAGTGGCACTAAGTATGCCCTCACTGCACTGACAGAGGACTCAGGC-AGAGCT 657
QY      663 TGGGAGGCGCCAGACCCACCATCCAGCCACGTGCTCTCCAGGTGTG-GTGAGACAC 721
Db      658 TCTGGAGGCGCCAGACCCATATCCG-GGCACGTGTATCTCTCCAGGCTTGGTAGAGAC 716
QY      722 AATTCGCCCTTCAACTCCAGCAGACAGCC-TGAGAAGGAGCTG-CAACTATGAGCA 779
Db      717 AGTTGCGCTTCAACTCCAGCAGACAGCCCGGCGAAGCGAGTCTGATACGTGTTAGCACA 776
QY      780 AAT-GAAGTGTCTCAAAACCCGAGGAGTGTGGCCGAGGCTGTAT-CTACGCTCTCAGCAC 837
Db      777 CTTACAGTGTCTCAGACCAGAGGAGCTGTCTGAGGCTGTATACGTGCTTAGCACA 836
QY      838 CCGCAGACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCAGGTGACCTAGTGA 897
Db      837 ACCCCACATGTGAGGCTTGGGACATCCAGATGAGGCCACAGACGAG--TGACTTATGT 894
QY      898 CTGTGGAGCTCTCTCTTC 916
Db      895 CTGTGGAGATCCTACTCC 913

RESULT 36
BM675954/c
LOCUS
DEFINITION
  UI-E-EJ0-ahf-o-21-0-UI-s1 UI-E-EJ0 Homo sapiens cDNA clone
  UI-E-EJ0-ahf-o-21-0-UI 3', mRNA sequence.
ACCESSION
  BM675954
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 570)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
  97044477
  8889548
  Contact: Soares, MB
  Coordinated Laboratory for Computational Genomics
  University of Iowa
  375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: Bento-soares@uiowa.edu
  Tissue Procurement: Dr. Gregg Hageman
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Dr. M. Bento Soares, University of Iowa
  Genetics (www.resgen.com).
  The following repetitive elements were found in this cDNA
  sequence: 1-38, >POLY_A#Simple_repeat (matched complement)
  Seq primer: M13 Forward
  POLYA=Yes.
FEATURES
  Location/Qualifiers
    1..570
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="UI-E-EJ0-ahf-o-21-0-UI"
      /tissue_type="fetal eyes, lens, eye anterior segment,
      optic nerve, retina, Retina Foveal and Macular, RPE and
      Choroid"
      /dev_stage="fetal and adult"

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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ0"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EJ0 is a subcloned cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AAGATCCAGA; lens, CGATTAGCGA; eye anterior segment,
AATGCCGAT; optic nerve, CCATTAGTGT; retina, CCGCG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACTTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI).
TAG_TISSUE=human retina
TAG_LIB=UI-E-EJ0
TAG_SEQ=CCGCG"

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ORIGIN

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Query Match      36.1%; Score 543; DB 12; Length 570;
Best Local Similarity 99.8%; Pred. No. 6.7e-86;
Matches 554; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      951 GGATTTAGGTGTGATTCTCTGGATCAGGATACCACTTCTGTCCACACCCGACAG 1010
Db      560 GGATTTAGGTGTGATTCTCTGGATCAGGATACCACTTCTGTCCACACCCGACAG 501
QY      1011 GGGCTAGAAAAATTTGTTTGAGATTTTATATCATCTTGTCAAATGCTTCAAGTTGTAAT 1070
Db      500 GGGCTAGAAAAATTTGTTTGAGATTTTATATCATCTTGTCAAATGCTTCAAGTTGTAAT 441
QY      1071 GTGAAAAATGGCTGGGGAAGAGGTGGTGCCTAATGTTTACTTGTAACTTGT 1130
Db      440 GTGAAAAATGGCTGGGGAAGAGGTGGTGCCTAATGTTTACTTGTAACTTGT 381
QY      1131 CTCTGCGCCCTGGGCACCTTGGCCCTTCTGCTCTCTGCTCTGCTCTTCCCTTTGACATGGGAA 1190
Db      380 CTCTGCGCCCTGGGCACCTTGGCCCTTCTGCTCTCTGCTCTTCCCTTTGACATGGGAA 321
QY      1191 AGGAGTTGTGCGCCAAAAATCCCACTTCTTTGCACTCAAGCTCTGTGGCTCAGGCTGGG 1250
Db      320 AGGAGTTGTGCGCCAAAAATCCCACTTCTTTGCACTCAAGCTCTGTGGCTCAGGCTGGG 261
QY      1251 GTGGCAGAGGAGGCGCTTACCTTATATCTGTGTGTATCCAGGGCTCCAGACTTCTTC 1310
Db      260 GTGGCAGAGGAGGCGCTTACCTTATATCTGTGTGTATCCAGGGCTCCAGACTTCTTC 201
QY      1311 CTCTGCGCTGCCCACTGCACTTCTCCCTTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCT 1370
Db      200 CTCTGCGCTGCCCACTGCACTTCTCCCTTATCTATCTCTCTCTCTCTCTCTCTCTCTCT 141
QY      1371 AGCTTTGGCTTCTTGTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1430
Db      140 AGCTTTGGCTTCTTGTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 82
QY      1431 CAGAACACAGGCGCTGGCCCGAGTGTGATTCATGTTGATCATTAATAAAAAAATCGCA 1490
Db      81 CAGAACACAGGCGCTGGCCCGAGTGTGATTCATGTTGATCATTAATAAAAAAATCGCA 22
QY      1491 ACCAAAAAATAAAAA 1505
Db      21 ACCAAAAAATAAAAA 7

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RESULT 37
 BG231973/c
 LOCUS
 DEFINITION

BG231973 541 bp mRNA linear EST 09-FEB-2001
 naf34g12.x1 Soares_NPBMc Homo sapiens cDNA clone IMAGE:414366 3',

mRNA sequence.
BG231973
BG231973.1 GI:12727118
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D. and M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Seq primer: -400P from Gibco
High quality sequence stop: 480.
Location/Qualifiers
1. 541
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/note="Organ: blood; Vector: pTV73D-Pac; Site 1: NotI;
Site 2: EcoRI; 1st strand cDNA was primed with a Not I -
oligo (dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGGCCGCCGGTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pTV73 vector. Library
is normalized; constructed in the laboratory of M. Bento
Soares (University of Iowa)."
FEATURES
source
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/lab_host="SNU-5"
/clone_lib="S1SNU5s1"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and
sequencing about 2,000 ~ 3,000 colonies in original cDNA

1312 TCTGCTGCCCCACTGCACCTCTCCCCCTATCTATCTCTTCTCGGCTCCCGAGCCCA 1371
181 TCTGCTGCCCCACTGCACCTCTCCCCCTATCTATCTCTTCTCGGCTCCCGAGCCCA 122
1372 GTCTTGCTTCTTGTGCTCCCTCTCCCTGCGGTCTATCCCTCCACTCTGACTCTGACTATGGCAGC 1431
121 GTCTTGCTTCTTGTGCTCCCTCTCCCTGCGGTCTATCCCTCCACTCTGACTCTGACTATGGCAGC 62
1432 AGAACACCGGGCTGGCCAGTGGATTTCATGATGATCAATTAATAAGAAAAATCGCAA 1491
61 AGAACACCGGGCTGGCCAGTGGATTTCATGATGATCAATTAATAAGAAAAATCGCAA 2
1492 C 1492
1 C 1
1 C 1
RESULT 38
BM743569
LOCUS
DEFINITION
K-EST0016711 S1SNU5s1 Homo sapiens cDNA clone S1SNU5s1-5-C01 5',
mRNA sequence.
ACCESSION
BM743569
VERSION
BM743569.1 GI:19064898
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 550)
AUTHORS
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE
21C Frontier Korean EST Project 2001
JOURNAL
Unpublished (2002)
COMMENT
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 5 row: C column: 01
High quality sequence stop: 550.
Location/Qualifiers
1. 550
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/sex="P"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/lab_host="SNU-5"
/clone_lib="S1SNU5s1"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and
sequencing about 2,000 ~ 3,000 colonies in original cDNA

library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(ΔT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the substracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells *E. coli* Top10⁺ with electroporation method."

ORIGIN

Query Match	35.8%;	Score 539;	DB 12;	Length 550;
Best Local Similarity	99.8%;	Pred. No. 3.4e-85;		
Matches 550;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;

QY	350	TGTTCTCAGCTATCGCTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGCT	409
Db	1	TGTTCTCAGCTATCGCTTCTCAGCAGCGGTGTAGACA-CTGCATCAACAATGCTGGCT	59
QY	410	TGCGCCGGCTGACACCTGCTCTCAGCAGCACCATGCTGGTGGAGGACATGTTCAATG	469
Db	60	TGCGCCGGCTGACACCTGCTCTCAGCAGCACCATGCTGGTGGAGGACATGTTCAATG	119
QY	470	TGAAGCTGTGGCTTCTCAGCATCTGCACACGGGAGCCTACCAGTCCATGAGGAGCGGA	529
Db	120	TGAAGCTGTGGCTTCTCAGCATCTGCACACGGGAGCCTACCAGTCCATGAGGAGCGGA	179
QY	530	ATGTGGAGCATGGGCATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCC	589
Db	180	ATGTGGAGCATGGGCATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCC	239
QY	590	TGCTGTGACCCACTTCTATAGTGACCAAGATATGCCGTACTCGCTGTACAGAGGAC	649
Db	240	TGCTGTGACCCACTTCTATAGTGACCAAGATATGCCGTACTCGCTGTACAGAGGAC	299
QY	650	TGAGGCAAGAGCTTGGGAGGCGCCAGACCCATCCAGGACCCGATCCGAGGACCGTGT	709
Db	300	TGAGGCAAGAGCTTGGGAGGCGCCAGACCCATCCGAGGACCCGATCCGAGGACCGTGT	359
QY	710	TGTTGGAGACCAATTCGCTTCAAACTCCAGCAAGGACCCCTGAGAGGCGAGTGCCA	769
Db	360	TGTTGGAGACCAATTCGCTTCAAACTCCAGCAAGGACCCCTGAGAGGCGAGTGCCA	419
QY	770	CCTATGAGCAATGAAGTGTCTCAACCCGAGGATGTGGCGAGGCTGTATCTACGTCC	829
Db	420	CCTATGAGCAATGAAGTGTCTCAACCCGAGGATGTGGCGAGGCTGTATCTACGTCC	479
QY	830	TCAGACCCCGGCACATCCAGATTCGAGACATCCAGATGAGGCCACCGAGCAGGTGA	889
Db	480	TCAGACCCCGGCACATCCAGATTCGAGACATCCAGATGAGGCCACCGAGCAGGTGA	539
QY	890	CCTAGTACCTG 900	
Db	540	CCTAGTACCTG 550	

RESULT 39
CA424831/c

LOCUS
CA424831 DEFINITION
UI-H-FEI-bdw-e-17-0-UI.s1 NCI CGAP FEI Homo sapiens cDNA clone
UI-H-FEI-bdw-e-17-0-UI 3', mRNA sequence.

ACCESSION
CA424831
VERSION
CA424831.1 GI:24787557
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 566)
AUTHORS
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE JOURNAL COMMENT

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=tes.

FEATURES source

1..566
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B (Life Technologies)"
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/note="Organ: Chondrosarcoma; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FEI is a normalized cDNA library derived from a pool of mRNA obtained from 3 cell lines from grade II chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genom Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dri)18 tail. The sequence tag for this library is CGCTACCGAC. The cell lines were provided by Dr James Martin from the University of Iowa.
TAG TISSUE=Human grade 2 chondrosarcoma cell line pool
TAG LIB=UI-H-FEI
TAG_SEQ=CGCTACCGAC"

ORIGIN

Query Match	35.4%;	Score 533;	DB 14;	Length 566;
Best Local Similarity	98.6%;	Pred. No. 3.9e-84;		
Matches 548;	Conservative 0;	Mismatches 6;	Indels 2;	Gaps 1;

QY	952	GAATTTAGTGTGATTTCTGGATCAGGGATACCACTTCTGTCACACCCGACGAGG	1011
Db	566	GAATTTAGTGTGATTTCTGGATCAGGGATACCACTTCTGTCACACCCGACGAGG	507
QY	1012	GGCTAGAAAAATTTGTTGAGATTTTATATCATCTTGTCAAAATGCTTCAGTTGTAATG	1071
Db	506	GGCTAGAAAAATTTGTTGAGATTTTATATCATCTTGTCAAAATGCTTCAGTTGTAATG	447
QY	1072	TGAAAAATGGCTGGGAAAGGAGGTGGTCCCTAAATGTTTACTTGTGTTAACTTCTC	1131
Db	446	TGAAAAATGGCTGGGAAAGGAGGTGGTCCCTAAATGTTTACTTGTGTTAACTTCTC	387
QY	1132	TTTGCCCTGGGCACTTGGCCCTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGAAA	1191
Db	386	TTTGCCCTGGGCACTTGGCCCTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGAAA	327
QY	1192	GGAGTTGTGSCCAAAATCCCACTTCTTGCACCTCAAGTCTGTGGCTCAGGGCTGGG	1251
Db	326	GGAGTTGTGSCCAAAATCCCACTTCTTGCACCTCAAGTCTGTGGCTCAGGGCTGGG	267
QY	1252	TGSCAGAGGAGGCGCTTACCTTATATCTGTGTGTATCCAGGGCTCCAGACTTCTCTC	1311
Db	266	TGSCAGAGGAGGCGCTTACCTTATATCTGTGTGTATCCAGGGCTCCAGACTTCTCTC	207
QY	1312	TTTGCTGCCCCACTGACACCTCTCCCTTATCTATCTCTCTTCTCGGCTCCCGACCGCA	1371

Db

206

TCCTGCTGCCCACTGACACCTCTCCCTTATCTATCTCTCGGCTCCCGAGCCA

147

QY

1372

GTCTTGACTTCTGCTCCCTCCCTGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGC

1431

Db

146

GTCTTGCTCTTGTGCTCCCTCCCTGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGC

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QY

1432

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1489

Db

86

AGAACACAGGGCTGGCCCACTGGATTTTCATGTGATCATTTAAAAAGAAAAATCGC

27

QY

1490

AACCAAAAAA 1505

Db

26

AACCAATCAAAAAA 11

RESULT 40

EX671560

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BX671560

612 bp

mRNA

linear

EST 24-OCT-2003

BX671560 Sus Scrofa library (scac) Sus scrofa cDNA clone

scac0032i.1.1.13 5prim, mRNA sequence.

BX671560

BX671560.1

GI:37983262

EST.

Sus scrofa (pig)

Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 612)

Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S., Soares,M., Bonaldo,F. and Hately,F.

A Pig Normalised Multi-Tissue cDNA Library

Unpublished (2003)

Contact: Tosser-Klopp G

Genetique Animale

Institut National de la Recherche Agronomique

Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan cedex, FRANCE

Tel: 33 (0) 5.61.28.51.14

Fax: 33 (0) 5.61.28.53.08

Email: tosser@toulouse.inra.fr

Clone distribution: AGENAE Resource centre, Francois PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73

Sequence cleaned of vector, adaptor and repetitions. Contact us at signasupport@jouy.inra.fr to obtain the chromatogram of this sequence.

Plate: 0032 row: 1 column: 13.

FEATURES

source

1. .612

Location/Qualifiers

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="scac0032i.1.13"

/tissue_type="mixed"

/clone_lib="Sus Scrofa library (scac)"

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ORIGIN

Query Match

Best Local Similarity

Matches

556; Conservative

0; Mismatches

39; Indels

0; Gaps

0;

QY

145

CGGCTGCGCTGGTACAGGGGGCTCGGGGGGCGATCGCGCGCGCGGGCCCTG

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Db

1

CGACTGGCACTGGTGACAGGAGCTCGGGGGGCGATCGCGCGCGCGGGCCCTG

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QY

205

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Db

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120

QY

265

GCTGCTCAATGTAAGAGTGCAGGCTACCCCGGGAATTTGATCCCTACAGATGACCTA

324

Db

121

GCCGCCAGTGTAAAGTGCAGGCTACCCCGGGAATTTGATCCCTACAAATGTGACCTG

180

QY

325

TCAAATGAAGAGGACATCTCTCCATGTTCTCAGTATCCGTTCTCAGCAGCGGTGTA

384

Db

181

TCAAATGAGGAGGACATCTCTCCATGTTCTCAGTATCCGTTCTCAGCAGCGGTGTA

240

QY

385

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444

Db

241

GACATCTGCATCAACAACGCGGCTTGGCCCGGCTGACACCCCTGCTCTCAGGAGCACC

300

QY

445

AGTGGTTGGAAGGACATGTTCAATGTGAACGTGTGGCCCTCAGCATCTGCACAGGGAA

504

Db

301

AGCGTTTGAAGGACATGTTCAATGTGAACGTGTGGCCCTCAGCATCTGCACAGGGAA

360

QY

505

GCCTACAGTCCATGAAGGAGCGGAATGTGACAGTGGCACATCAATCAATCAATAGC

564

Db

361

GCCTACAGTCCATGAAGGAGCGGAATGTGACAGTGGCACATCAATCAATCAATAGC

420

QY

565

ATGTCTGCCACCGAGTGTACCCCTGCTCTGTGACCCCACTTCTATAGTGCACCAAGTAT

624

Db

421

ATGTCTGCCACCGAGTGTACCCCTGCTCTGTGACCCCACTTCTATAGTGCACCAAGTAT

480

QY

625

GCCGTCACCTGCGCTGACAGAGGAGCTAGGCAAGAGCTTCGGGAGGCCAGCCACATC

684

Db

481

GCCGTCACCTGCGCTGACAGAGGAGCTAGGCAAGAGCTTCGGGAGGCCAGCCACATC

540

QY

685

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Db

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595

RESULT 41

BG037061

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

602288368F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4374184 5',

mRNA sequence.

BG037061

BG037061.1

GI:12432922

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 751)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshituki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLAM10037 row: g column: 17

High quality sequence stop: 687.

FEATURES

source

1. .751

Location/Qualifiers

/organism="Homo sapiens"

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/clone="IMAGE:4374184"

/lab_host="DH10B"

/clone_lib="NIH_MGC_97"
 /notes="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 35.4%; Score 532.6; DB 10; Length 751;
 Best Local Similarity 96.6%; Pred. No. 4.5e-84;
 Matches 598; Conservative 0; Mismatches 14; Indels 7; Gaps 5;

QY 1 CGCGATCGGACCCAGCAGGTGCGCGCGCGGAGGAGCGCGCGGCTCAGCTCC 60
 Db 107 CGCGATCGGACCCAGCAGGTGCGCGCGCGGAGGAGCGCGCGGCTCAGCTCC 166
 QY 61 TCGACCCCGGTGCGCGGTAGTCCAGCGAGGCGGAGCGCGGCTCAGCTCC 120
 Db 167 TCGACCCCGGTGCGCGGTAGTCCAGCGAGGCGGAGCGCGGCTCAGCTCC 226
 QY 121 CCGGATCGGACCCAGCAGGTGCGCGCGCGGAGGAGCGCGCGGCTCAGCTCC 180
 Db 227 CCGGATCGGACCCAGCAGGTGCGCGCGCGGAGGAGCGCGCGGCTCAGCTCC 286
 QY 181 GCGCGCGCGGTGCGCGGCTGAGTCCAGCGAGGAGCGCGGCTCAGCTCC 240
 Db 287 GCGCGCGCGGTGCGCGGCTGAGTCCAGCGAGGAGCGCGGCTCAGCTCC 346
 QY 241 ACTGTGGCAACATCGAGGAGTGGCTGAGTCCAGCGAGGAGCGCGGCTCAGCTCC 300
 Db 347 ACTGTGGCAACATCGAGGAGTGGCTGAGTCCAGCGAGGAGCGCGGCTCAGCTCC 406
 QY 301 TTGATCCCTACAGATGTGACCTATCAATGAAGAGGACATCTCTCCATGTTCTCAGCT 360
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 Db 467 ATCCGTTCTCAGCAGCGGTGAGATCTGCATCAACATGCTGGCTGGCGCGGCT 525
 QY 421 GACACCTGCTCTCAGCAGCAGCAGTGG-TTGAAGGACATGTTCAATGTGAACGTGCT 479
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 QY 480 GGGCCTCAGCATCTGCACAGGAGGCTTACAGTCCATG-AAAGAGCGGAATGTGGACG 538
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 QY 539 ATGGGACATCAATTAACATCAATAGATGTGTGGCCACCGAGTGTACCCCTGTCTGTGA 598
 Db 646 ATGGGACATCAATTAATATC-ATAGCATGTGTGGCCACCGAGTGTACCCCTGTCTGTGA 701
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 Db 702 ACCACTTCTATAGTGCCAC 720

RESULT 42
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 VERSION BI546418.1 GI:15433730
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 714)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: c9apbs@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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FEATURES

source

ORIGIN

Query Match 35.2%; Score 530.2; DB 12; Length 714;
 Best Local Similarity 86.1%; Pred. No. 1.2e-83;
 Matches 678; Conservative 0; Mismatches 3; Indels 106; Gaps 4;

QY 1 CGCGATCGGACCCAGCAGGTGCGCGCGCGGAGGAGCGCGCGGCTCAGCTCC 60
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 Db 78 TCGACCCCGGTGCGCGGTAGTCCAGCGAGGCGGAGCGCGGCTCAGCTCC 137
 QY 121 CCGGATCGGACCCAGCAGGTGCGCGCGCGGAGGAGCGCGCGGCTCAGCTCC 180
 Db 138 CCGGATCGGACCCAGCAGGTGCGCGCGCGGAGGAGCGCGCGGCTCAGCTCC 170
 QY 181 GCGCGCGCGGTGCGCGGCTGAGTCCAGCGAGGAGCGCGGCTCAGCTCC 240
 Db 171 GCGCGCGCGGTGCGCGGCTGAGTCCAGCGAGGAGCGCGGCTCAGCTCC 209
 QY 241 ACTGTGGGCAACATCGAGGAGTGGCTGATGATGAAGAGTGCAGGCTACCCCGGACT 300
 Db 210 ACTGTGGGCAACATCG----- 225
 QY 301 TTGATCCCTACAGATGTGACCTATCAATGAAGAGGACATCTCTCCATGTTCTCAGCT 360
 Db 226 -----AGATGTGACCTATCAATGAAGAGGACATCTCTCCATGTTCTCAGCT 273
 QY 361 ATCCGTTCTCAGCAGCGGTGAGACATCTGCA-TCACAAATGTGGCTTGGCCCGGCC 419
 Db 274 ATCCGTTCTCAGCAGCGGTGAGACATCTGCA-TCACAAATGTGGCTTGGCCCGGCC 333
 QY 420 TGACACCCCTGCTCTCAGGAGCAGCAGTGGTTGGAGGACATGTTCAATGTGAACGTGCT 479
 Db 334 TGACACCCCTGCTCTCAGGAGCAGCAGTGGTTGGAGGACATGTTCAATGTGAACGTGCT 393

AUTHORS
 TITLE
 NC1-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 COMMENT
 Contact: Robert Strausberg, Ph. D.
 Email: cgapps@mail.nih.gov
 This clone is available royalty-free through LINL : contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 675 Std Error: 0.00
 Seq primer: ~40UP from Gibco
 High quality sequence stop: 470.

Db	421	CCAAATCCCATCTTCTTGACCTCAACGTCCTGGCTCAGGCTGGGTGGCAGANGG	480
Qy	1262	AGGCCTTCACTTATATCTGTGTTATCCAG	1294
Db	481	AGGCCTTCACTTATATCTGTGTTATCCAG	513
RESULT 46			
LOCUS	B1260323	546 bp	mRNA linear EST 17-JUL-2001
DEFINITION	602969342F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5108699 5',		
ACCESSION	B1260323	mRNA sequence.	
VERSION	B1260323.1	GI:14818515	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1	(bases 1 to 546)	
AUTHORS	NIH-MGC	http://mgs.nci.nih.gov/.	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11263 row: d column: 12 High quality sequence stop: 546.		
FEATURES			
source		Location/Qualifiers	
1..546		/organism="Homo sapiens"	
		/mol_type="mRNA"	
		/db_xref="taxon:9606"	
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		/tissue_type="cervical carcinoma cell line"	
		/lab_host="DH10B"	
		/clone_lib="NIH_MGC_12"	
		/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.4 kb. Library prepared by Life Technologies."	
ORIGIN			
Query Match		33.9%; Score 509.8; DB 12; Length 546;	
Best Local Similarity		98.3%; Pred. No. 4.9e-80;	
Matches 536; Conservative		0; Mismatches 7; Indels 2; Gaps 2;	
Qy	962	GTGTATTCTGATCAGGGATACACCTTCCTGTCACACCCCGACCGGGCTAGAAA	1021
Db	1	GTGTATTCTGATCAGGGATACACCTTCCTGTCACACCCCGACCA-GGGCTAGAAA	59
Qy	1022	TTTGTTCAGATTTTATATCATCTTGTCAAAATGCTTCAGTTGTAATGTGAAAAATGG	1081
Db	60	TTTGTTCAGATTTTATATCATCTTGTCAAAATGCTTCAGTTGTAATGTGAAAAATGG	119
Qy	1082	GCTGGGAAAGAGGTGGTGCCTTAATGTTTACTTGTAACTGTTCTTGTCGCCCT	1141
Db	120	GCTGGGAAAGAGGTGGTGCCTTAATGTTTACTTGTAACTGTTCTTGTCGCCCT	179
Qy	1142	GGGCACTTGGCTTTGTCTGCTCTCAGTCTCTTCCCTTTGACATGGGAAGAGTTGTGG	1201
Db	180	GGGCACTTGGCTTTGTCTGCTCTCAGTCTCTTCCCTTTGACATGGGAAGAGTTGTGG	239
Qy	1202	CCAAAAATCCCATCTTCTTGACCTCAACGTCGTGTGGCTCAGGG-CTGGGGTGGCAGAGG	1260
Db	240	CCAAAAATCCCATCTTCTTGACCTCAACGTCGTGTGGCTCAGGGNCTGGGGTGGCAGAGG	299

Qy	1261	GAGGCTTCACTTATATCTGTGTTTATCCAGGCTCCAGACTTCTCTCTGCTGCTGC	1320
Db	300	GAGGCTTCACTTATATCTGTGTTTATCCAGGCTCCAGACTTCTCTCTGCTGCTGC	359
Qy	1321	CCCACTGCACCTCTCCCTCTTATCTATCTCTTCTCGGCTCCCGACCGAGTTGGCT	1380
Db	360	CCCACTGCACCTCTCCCTCTTATCTATCTCTTCTCGGCTCCCGACCGAGTTGGCT	419
Qy	1381	TCCTGTCCTCTCTGGGGTCATCCCTCCTCTGACTCTGACTATGGCAGCAGAACCA	1440
Db	420	TCCTGTCCTCTCTGGGGTCATCCCTCCTCTGACTCTGACTATGGCAGCAGAACCA	479
Qy	1441	GGGCTGGCCAGTGGATTTCATGCTGATCATTAATAAAGAAAAATCGCAACCAAAAA	1500
Db	480	GGGCTGGCCAGTGGATTTCATGCTGATCATTAATAAAGAAAAATCGCAACCAAAAA	539
Qy	1501	AAAAA 1505	
Db	540	AAAAA 544	
RESULT 47			
LOCUS	BE962188	716 bp	mRNA linear EST 14-DEC-2000
DEFINITION	601655404R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846168 3',		
ACCESSION	BE962188	mRNA sequence.	
VERSION	BE962188.2	GI:11764835	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1	(bases 1 to 716)	
AUTHORS	NIH-MGC	http://mgs.nci.nih.gov/.	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	On Oct 3, 2000 this sequence version replaced gi:10572893. Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM545 row: g column: 01 High quality sequence stop: 704.		
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		/clone="IMAGE:3846168"	
		/tissue_type="adenocarcinoma"	
		/lab_host="DH10B (phage-resistant)"	
		/clone_lib="NIH_MGC_65"	
		/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."	
ORIGIN			
Query Match		33.7%; Score 506.6; DB 10; Length 716;	
Best Local Similarity		93.2%; Pred. No. 1.8e-79;	
Matches 653; Conservative		0; Mismatches 29; Indels 19; Gaps 11;	
Qy	823	TACGTCCTCAGCACCCCGCACATCCAGATTGGAGATCCAGATCAGATGAGGCCCGGA-	881
Db	704	TACGTCCTCAGCACCCCGCACATCCAGATTGG-GACATCCAGATGAGGCCCGGAG	646

QY 882 GCAGTGACCTAGTGTGGAGCTCTCTCTT--CCCTCCCAACCCCTTCATGGCTTCG 939
 Db 645 GCAGTGACCTAGTGTGGAGCTCTCTCTTCCCTCGCCACCCCTTCATGGCTTCG 586
 QY 940 CTCCTGCTCTGATTTTA-GGTGTTGATTTCTGGATCAGGGATACCACTTCCTGT--C 996
 Db 585 CTCCTGCTCTGATTTTAAGGTGTTGAATTTCTGGATCAGGGATACCACTTCCTGTTCG 526
 QY 997 CACACCCGACCA-GGGGCTAGAAAATTTGTTTGAGATTTTATATCATCTTGTCAAAAT 1055
 Db 525 CACACCCGACCAAGGGCTAGAAAATTTGTTTGAGATTTTATATCATCTTGTCAAAAT 466
 QY 1056 GCTTCAGTTGTAAA---TGTGAAAAATGGGCTGGGAAAGAGGTGCTCCCTAATTTG 1112
 Db 465 GCTTCAGTTGTAAAATGTCAAAATTTGGGCTGGGAAAGAGGTGCTCCCTAATTTG 406
 QY 1113 TTTACTTGTAACTTGTCTTGTGCTCCCTGGGCACTTGGCCCTTGTCTCTCAGTGTG 1172
 Db 405 TTTACTTGTAACTTGTCTTGTGCTCCCTGGGCACTTGGCCCTTGTCTCTCAGTGTG 346
 QY 1173 TTCCCTTT---GACATGGGAAAGAGTTGTGGCCAAAATCCCAATCTCTTGGACCTCA 1228
 Db 345 TTCCCTATTGACATGGGAAAGAGTTGTGGCCAAAATCCCAATCTCTTGGACCTCA 286
 QY 1229 ACCTCTGTGGCTCAGGCTGGGCTGGGAGAGGAGGCTTCACTTAT--ATCTGTGTG 1286
 Db 285 ACCTCTGTGGCTCAGGCTGGGCTGGGAGAGGAGGCTTCACTTATATAATCTGTGTG 226
 QY 1287 TTA-TCCAGGCTCCAGACTTCTCTCTGCTGCTGCCCACTGCACCTCTCCCTTATC 1345
 Db 225 TTAGTCCAGGCTCCAGACTTCTCTCTGCTGCTGCCCACTGCACCTCTCCCTTATC 166
 QY 1346 TATCTCTCTCTGGCTCCCAAGCCAGCTTGGCTTCTTGTGCTTCTGCTCCCTGCTCC 1405
 Db 165 TATCTCTCTCTGGCTCCCAAGCCAGCTTGGCTTCTTGTGCTTCTGCTCCCTGCTCC 106
 QY 1406 TCCACTCTGACTCTGACTATGGCAGCAGAACACAGGCGCTGGGCCAG-TGGATTTCATG 1464
 Db 105 TCCACTCTGACTCTGACTATGGCAGCAGAACACAGGCGCTGGGCCAGTGGATTTCATG 46
 QY 1465 GTGATCATTAAGAAAGAAATCGCAACCAAAAAA 1505
 Db 45 GTGATCATTAAGAAAGAAATCGCAACCAAAAAA 5

AL559035 976 bp mRNA linear EST 31-MAY-2003
 AL559035 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
 Homo sapiens cDNA clone CS0DJ010YN13 3-PRIME, mRNA sequence.
 AL559035
 EST.
 AL559035.2 GI:31283168
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:12904136.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 8845.f For more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DJ010CG07NP1&cluster=8845.f. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DJ010CG07NP1.
 Location/Qualifiers
 1..976
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DJ010YN13"
 /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
 /cell_line="JURKAT"
 /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
 ORIGIN
 Query Match 33.5%; Score 504.2; DB 9; Length 976;
 Best Local Similarity 98.8%; Pred. NO. 4.6e-79;
 Matches 504; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 920 CCCACCCCTTCATGCTTGCCTCCTGCTCTGGATTTTAGGTGTGATTTCTGGATCAG 979
 Db 510 CCCACCCCTTCATGCTTGCCTCCTGCTCTGGATTTTAGGTGTGATTTCTGGATCAG 451
 QY 980 GGATACCACTTCCTGTCCACACCCCGACAGGGGCTAGAAAATTTGTTGAGATTTTAT 1039
 Db 450 GGATACCACTTCCTGTCCACACCCCGACAGGGGCTAGAAAATTTGTTGAGATTTTAT 391
 QY 1040 ATCATCTGTCAAAATGCTTCAGTTGTAATGTGAAAATGGGCTGGGAAAGGAGGTGG 1099
 Db 390 ATCATCTGTCAAAATGCTTCAGTTGTAATGTGAAAATGGGCTGGGAAAGGAGGTGG 331
 QY 1100 TGTCCCTAAATGTTTACTTCTTAACCTTGTGCTCCCTGGCCCTGGCACTTGGCTTGTG 1159
 Db 330 TGTCCCTAAATGTTTACTTCTTAACCTTGTGCTCCCTGGCCCTGGCACTTGGCTTGTG 271
 QY 1160 TGTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCACTTCT 1219
 Db 270 TGTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCACTTCT 211
 QY 1220 TGCACCTCAAGCTGTGGCTCAGGCTGGGTGGGAGAGGAGGCTTACCTTATATC 1279
 Db 210 TGCACCTCAAGCTGTGGCTCAGGCTGGGTGGGAGAGGAGGCTTACCTTATATC 151
 QY 1280 TGTGTTGTTATCAGGGCTCCAGACTTCTCCCTGCTGCTCCCTGCACTGCACTTCCCC 1339
 Db 150 TGTGTTGTTATCAGGGCTCCAGACTTCTCCCTGCTGCTCCCTGCACTGCACTTCCCC 91
 QY 1340 CTATCTATCTCTTCTCGGCTCCCAAGCCAGTCTTGGCTTCTTGTCCCTCTCTGGGT 1399
 Db 90 NBTATVTATCTCTTCTCGGCTCCCAAGCCAGTCTTGGCTTCTTGTCCCTCTCTGGGT 31
 QY 1400 CATCCCTCCACTCTGACTCTGACTATGGCA 1429
 Db 30 CATCCCTCCACTCTGACTCTGACTATGGCA 1

RESULT 49
 BF233600
 LOCUS
 DEFINITION
 602024015F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4159658 5', mRNA sequence.
 BF233600
 ACCESSION
 BF233600.1 GI:11144177
 VERSION
 EST.
 KEYWORDS
 Mus musculus (house mouse)
 SOURCE
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 881)
 REFERENCE
 NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)

646 GAGGGGACTCAGCAAGAGGCTTCGAGGAGCCAGACCCATATTCGGGGCCACGTCGTATCTC 703
 702 TCCAGGCTGTGGTGGAGACACAAATTCGCTTCAAATCCACGACCAAGACCCCTGAGAAG 759
 706 TCCAGGCTGTGTAGACACACAGTTCGCTTCAAATCATGACAAACGTACCCGGGGAAG 763
 W58459 536 bp mRNA linear EST 15-OCT-1996
 zd25h06.s1 Soares fetal heart NBHH19W Homo sapiens cDNA clone
 IMAGE:341723 3', mRNA sequence.
 W58459.1 GI:1365172
 EST.
 W58459 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 536)
 Haller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Hollman,M., Huilman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevasaki,E., Waterston,R., Williamson,A., Wohlmann,P. and
 Wilson,R.
 The WashU-Merck EST Project
 Unpublished (1995)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1349 Std Error: 0.00
 Seq primer: mob.REGA+ET
 High quality sequence stop: 420.
 Location/Qualifiers
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 /clone_lib="Soares fetal heart NBHH19W"
 /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer (5'
 TGTACCAATCTAGTGGGAGCGGCCGACATCTTTTCTTTTCTTTT 3'),
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by
 M.Fatima Bonaldo. This library was constructed from the
 same fetus as the fetal lung library, Soares fetal lung
 NBH19W."

Query Match 32.9%; Score 495.2; DB 14; Length 536;
 Best Local Similarity 98.5%; Pred. No. 1,9e-77;
 Matches 530; Conservative 0; Mismatches 5; Indels 3; Gaps 3

956 TTAGGTGTTGATTTCTGGATCAGCGGATACCACTTCTCTTCACACCCCGACGAGGGCT 1071
 535 TTAAGGTGTTGATTTCTGGATCAGCGGATACCA-TTCCTCTCCACACCCCGACGAGGGCT 1077
 1016 AGAATATTTGTTGAGATTTTATATCATCTTGTCAAATGCTTCAGTTGTAATATGTAA 1077

RESULT 50
 W58459/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

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Db      476 AGAAATTTGTTGAGATTTTATATCACTCTGCAAAITGCTTCAGTTGTAATGTGAA 417
QY      1076 AAATGGGCTGGGAAAGAGGTGGTGTCCCTAATCTGTTTACTTTGTTAACTTGTCTTGT 1135
Db      416 AAATGGGCTGGGAAAGAGGTGGTGTCCCTAATCTGTTTACTTTGTTAACTTGTCTTGT 357
QY      1136 GCGCTGGGCACTGTGGCCCTTGTCTCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAG 1195
Db      356 GCGCTGGGCACTGTGGCCCTTGTCTCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAG 297
QY      1196 TTGTGGCCAAATCCCATCTTCTTGACACCTCAACGTCTGTGGCTCAGGGCTGGGTGGC 1255
Db      296 TTGTGGCCAAATCCCATCTTCTTGACACCTCAACGTCTGTGGCTCAGGGCTGGGTGGC 237
QY      1256 AGAGGAGGCGCTTCACTTATATCTGTGTGTATCCAGGGCTCCAGACTTCTCTCTG 1315
Db      236 AGAGGAGGCGCTTCACTTATATCTGTGTGTATCCAGGGCTCCAGACTTCTCTCTG 177
QY      1316 CCTGCCCACTGCACCGCTCTCCCGCTTATCTATCTCTCTCGGCTCCCGCCAGTCT 1375
Db      176 CCTGCCCACTGCACCGCTCTCCCGCTTATCTATCTCTCTCGGCTCCCGCCAGTCT 117
QY      1376 TGGCTTCTGTCTCCCTCTGGGTGATCCCTCCACTCTGACTCTGACTATGGCAGAGAA 1435
Db      116 TGGCTTCTGT-CCCTCTGGGTGATCCCTCCACTCTGACTCTGACTATGGCAGAGAA 58
QY      1436 CACCAAGGCGCTGGCCAGTGGATTTTCATGGTGATCATTAATAAAGAAAAATCGCAACC 1493
Db      57 CACCA-GGCGTGGCCAGTGGATTTTCATGGTGATCATTAATAAAGAAAAATCGCAACC 1
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Search completed: September 16, 2004, 13:45:13
Job time : 3672 secs

B/ank

; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 89
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-89

Query Match 29.6%; Score 445; DB 4; Length 569;
Best Local Similarity 100.0%; Pred. No. 7e-198;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 998 ACACCCCGACGAGGGCTAGAAAATTTGTTGAGATTTTATCATCTTGTCAATGTC 1057
Db 42 ACACCCCGACGAGGGCTAGAAAATTTGTTGAGATTTTATCATCTTGTCAATGTC 101
QY 1058 TTCAGTTGTAATGTGAAATATGGCTGGGAAAGAGGTGGTGTCCCTAATTTGTTTAC 1117
Db 102 TTCAGTTGTAATGTGAAATATGGCTGGGAAAGAGGTGGTGTCCCTAATTTGTTTAC 161
QY 1118 TTGTTAACTTGTCTTGTGCCCTGGGCACTTGGCCTTGTCTGCTCAGTGTCTTCCC 1177
Db 162 TTGTTAACTTGTCTTGTGCCCTGGGCACTTGGCCTTGTCTGCTCAGTGTCTTCCC 221
QY 1178 TTGATCGGAAAGAGGTGGGCAAAATCCCATCTTCTTGACCTCAACGTCGTG 1237
Db 222 TTGATCGGAAAGAGGTGGGCAAAATCCCATCTTCTTGACCTCAACGTCGTG 281
QY 1238 GCTCAGGCTGGGTGGCAGAGGAGGCTTACCTTATATCTGTGTTGTTATCAGGCG 1297
Db 282 GCTCAGGCTGGGTGGCAGAGGAGGCTTACCTTATATCTGTGTTGTTATCAGGCG 341
QY 1298 TCCAGACTTCCTCTCTGCTGCCCACTGCACCTCTCCCTTATCTATCTCTCTC 1357
Db 342 TCCAGACTTCCTCTCTGCTGCCCACTGCACCTCTCCCTTATCTATCTCTCTC 401
QY 1358 GCTCTCCCGACCCAGTCTTGGCTTCTTGTCCTCTCTGGGGTCATCCCTCCACTCTGACT 1417
Db 402 GCTCTCCCGACCCAGTCTTGGCTTCTTGTCCTCTCTGGGGTCATCCCTCCACTCTGACT 461
QY 1418 CTGACTATGGCAGCAACACGAG 1442
Db 462 CTGACTATGGCAGCAACACGAG 486

RESULT 2

US-09-370-838-172
; Sequence 172, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Roadoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 172
; LENGTH: 608
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-370-838-172

Query Match 1.3%; Score 19; DB 4; Length 608;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1131 CTTGTGCCCCCTGGGCACCTT 1149
Db 459 CTTGTGCCCCCTGGGCACCTT 477

RESULT 3

US-09-489-039A-1571
; Sequence 1571, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 1571
; LENGTH: 672
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1571

Query Match 1.3%; Score 19; DB 4; Length 672;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 CGGACCGGCTGGCGCTGG 157
Db 352 CGGACCGGCTGGCGCTGG 370

RESULT 4

US-09-418-710-28
; Sequence 28, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710

; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 5561
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (346)...(4926)
US-09-418-710-28

Query Match 1.3%; Score 19; DB 4; Length 5561;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1471 ATTAAAAAGAAAAAATCGC 1489
Db 4993 ATTAAAAAGAAAAAATCGC 5011

RESULT 5
US-09-418-710-30
; Sequence 30, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 5573
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (346)...(4938)
US-09-418-710-30

Query Match 1.3%; Score 19; DB 4; Length 5573;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1471 ATTAAAAAGAAAAAATCGC 1489
Db 5005 ATTAAAAAGAAAAAATCGC 5023

RESULT 6
US-09-566-921-118
; Sequence 118, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US

; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 5702
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 025595.15
US-09-566-921-118

Query Match 1.3%; Score 19; DB 4; Length 5702;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1131 CTTGTGCCCTGGGCACCTT 1149
Db 3087 CTTGTGCCCTGGGCACCTT 3105

RESULT 7
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 1.3%; Score 19; DB 3; Length 4403765;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 138 GCGGACCGGCTGGCGCTG 156
Db 272023 GCGGACCGGCTGGCGCTG 272005

RESULT 8
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match
Best Local Similarity 1.3%; Score 19; DB 3; Length 4411529;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 138 GCGGACCGCTGGCGTG 156
Db 271911 GCGGACCGCTGGCGTG 271893

RESULT 9
US-09-621-976-10901
; Sequence 10901, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 10901
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-10901

Query Match
Best Local Similarity 1.2%; Score 18; DB 4; Length 375;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 952 GATTTAGGTTGATTT 969
Db 310 GATTTAGGTTGATTT 327

RESULT 10
US-08-960-022-1
; Sequence 1, Application US/08960022
; Patent No. 5976837
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,022
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1117 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-960-022-1

Query Match
Best Local Similarity 1.2%; Score 18; DB 2; Length 1117;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1488 GCAACCAAAAAAAAAA 1505
Db 1097 GCAACCAAAAAAAAAA 1114

RESULT 11
US-09-489-039A-2413
; Sequence 2413, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2413
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2413

Query Match
Best Local Similarity 1.2%; Score 18; DB 4; Length 1278;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 GGTGCGCGCGCGCGCAG 37
Db 153 GGTGCGCGCGCGCGCAG 170

RESULT 12
US-09-328-352-3222
; Sequence 3222, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 3222
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
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US-09-328-352-3222
Query Match      1.2%; Score 18; DB 4; Length 1413;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1469 TCATTAAAAAGAAAAAT 1486
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Db 1358 TCATTAAAAAGAAAAAT 1375

RESULT 13
US-09-266-225D-7/c
; Sequence 7, Application US/09266225D
; Patent No. 6573364
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishan
; APPLICANT: Kingsmore, Stephen
; APPLICANT: Tchernev, Velizar
; TITLE OF INVENTION: Isolation and Characterization of Hermansky-Pudlak
; TITLE OF INVENTION: Syndrome (HPS) Protein Complexes and HPS Protein-
; TITLE OF INVENTION: Interacting Proteins
; FILE REFERENCE: 15966-523
; CURRENT APPLICATION NUMBER: US/09/266,225D
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1730
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-266-225D-7

Query Match      1.2%; Score 18; DB 4; Length 1730;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1488 GCAACCAAAAAAAAAA 1505
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Db 1564 GCAACCAAAAAAAAAA 1547

RESULT 14
US-09-491-522-6/c
; Sequence 6, Application US/09491522
; Patent No. 6428998
; GENERAL INFORMATION:
; APPLICANT: Colige, Alain
; APPLICANT: Lapierre, Charles M.
; APPLICANT: Prockop, Darwin J.
; TITLE OF INVENTION: RECOMBINANT N-PROTEINASE.
; TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/491,522
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/886,333
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
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NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389-0060-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2023 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-491-522-6

Query Match      1.2%; Score 18; DB 4; Length 2023;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CGCGCGCGCGCGCAGGAG 40
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Db 177 CGCGCGCGCGCGCAGGAG 160

RESULT 15
US-09-599-360B-55
; Sequence 55, Application US/09599360B
; Patent No. 6548633
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bougueleret, L.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: GENSET.050CP3
; CURRENT APPLICATION NUMBER: US/09/599,360B
; CURRENT FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/141,032
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/469,099
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO 55
; LENGTH: 2356
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 42..1097
; NAME/KEY: sig_peptide
; LOCATION: 42..110
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.40
; NAME/KEY: polyA_signal
; LOCATION: 2323..2328
; NAME/KEY: polyA_site
; LOCATION: 2341..2356
US-09-599-360B-55

Query Match      1.2%; Score 18; DB 4; Length 2356;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1488 GCAACCAAAAAAAAAA 1505
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Db 2335 GCAACCAAAAAAAAAA 2352

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Job time : 149 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 16, 2004, 10:29:05 ; Search time 740 Seconds

(without alignments)
10265.415 Million cell updates/sec

Title: US-10-063-735-127

Perfect score: 1505

Sequence: 1 cgcggatcgaccacagcag.....tcgcaaccccaaaaaaaaaa 1505

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Searched: 3327077 seqs, 2523723180 residues

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Minimum DB seq length: 0

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Database : Published Applications NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1505	100.0	1505	13	US-10-206-915-377
2	1505	100.0	1505	13	US-10-199-670-377
3	1505	100.0	1505	13	US-10-201-858-377
4	1505	100.0	1505	13	US-10-205-890-377
5	1505	100.0	1505	13	US-10-208-024-377
6	1505	100.0	1505	13	US-10-201-853-377
7	1505	100.0	1505	13	US-10-063-745-127
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12	1505	100.0	1505	13	US-10-174-581-377
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15	1505	100.0	1505	13	US-10-176-914-377	Sequence 377, App
16	1505	100.0	1505	13	US-10-176-915-377	Sequence 377, App
17	1505	100.0	1505	13	US-10-063-555-127	Sequence 127, App
18	1505	100.0	1505	13	US-10-063-563-127	Sequence 127, App
19	1505	100.0	1505	13	US-10-063-594-127	Sequence 127, App
20	1505	100.0	1505	13	US-10-063-553-127	Sequence 127, App
21	1505	100.0	1505	13	US-10-063-554-127	Sequence 127, App
22	1505	100.0	1505	13	US-10-176-484-377	Sequence 377, App
23	1505	100.0	1505	13	US-10-180-550-377	Sequence 377, App
24	1505	100.0	1505	13	US-10-183-014-377	Sequence 377, App
25	1505	100.0	1505	13	US-10-187-738-377	Sequence 377, App
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33	1505	100.0	1505	13	US-10-195-896-377	Sequence 377, App
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36	1505	100.0	1505	13	US-10-196-757-377	Sequence 377, App
37	1505	100.0	1505	13	US-10-197-704-377	Sequence 377, App
38	1505	100.0	1505	13	US-10-197-710-377	Sequence 377, App
39	1505	100.0	1505	13	US-10-198-758-377	Sequence 377, App
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42	1505	100.0	1505	13	US-10-199-309-377	Sequence 377, App
43	1505	100.0	1505	13	US-10-199-313-377	Sequence 377, App
44	1505	100.0	1505	13	US-10-199-456-377	Sequence 377, App
45	1505	100.0	1505	13	US-10-201-329-377	Sequence 377, App

ALIGNMENTS

RESULT 1

US-10-206-915-377

; Sequence 377, Application US/10206915

; Publication No. US20040029221A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C513

; CURRENT APPLICATION NUMBER: US/10/206,915

; CURRENT FILING DATE: 2002-07-26

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

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Db	1201	GCCAAATCCCCATCTCTTGACACCTCAACGCTCTGTGGCTCAGGGCTGGGGTGGCAGAGG	1260	
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Db	1261	GAGGCTTCACTTATATCTGTGTGTTATCCAGGGCTCCAGACTTCTCTCTGCTGCTGC	1320	
Qy	1321	CCCACTGCACTCTCCGCCCTTATCTATCTCTCTCGGCTCCCGACCCAGTCTTGGCT	1380	
Db	1321	CCCACTGCACTCTCCGCCCTTATCTATCTCTCTCGGCTCCCGACCCAGTCTTGGCT	1380	
Qy	1381	TCCTGTCCTCCCTCGTGGGCTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACCA	1440	
Db	1381	TCCTGTCCTCCCTCGTGGGCTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACCA	1440	
Qy	1441	GGGCTGGCCAGTGGATTTTCATGGTGATCATTTAAAAAGAAAAATCGAACCAAAAAA	1500	
Db	1441	GGGCTGGCCAGTGGATTTTCATGGTGATCATTTAAAAAGAAAAATCGAACCAAAAAA	1500	
Qy	1501	AAAAA 1505		
Db	1501	AAAAA 1505		
RESULT 2				
US-10-199-670-377				
; Sequence 377, Application US/10199670				
; Publication No. US20040033560A1				
; GENERAL INFORMATION:				
; APPLICANT: Baker, Kevin P.				
; APPLICANT: Chen, Jian				
; APPLICANT: Desnoyers, Luc				
; APPLICANT: Goddard, Audrey				
; APPLICANT: Godowski, Paul J.				
; APPLICANT: Gurney, Austin L.				
; APPLICANT: Pan, James				
; APPLICANT: Smith, Victoria				
; APPLICANT: Watanabe, Colin K.				
; APPLICANT: Wood, William I.				
; APPLICANT: Zhang, Zemin				
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC				
; TITLE OF INVENTION: ACIDS ENCODING THE SAME				
; FILE REFERENCE: P3430R1C401				
; CURRENT APPLICATION NUMBER: US/10/199,670				
; CURRENT FILING DATE: 2002-07-19				
; PRIOR APPLICATION NUMBER: 10/052586				
; PRIOR FILING DATE: 2002-01-15				
; PRIOR APPLICATION NUMBER: 60/059263				
; PRIOR FILING DATE: 1997-09-18				

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; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-199-670-377

Query Match      100.0%; Score 1505; DB 13; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGATCGGACCCAGAGAGGTGCGCGGCGGCGGAGAGAGCGCGCGGTCTAGCTCC 60
Db 1 CGCGGATCGGACCCAGAGAGGTGCGCGGCGGCGGAGAGAGCGCGCGGTCTAGCTCC 60

QY 61 TCGACCCCGGTGTCGGGCTAGTCAGAGCGAGCGAGCGCGCGGTGAGAGAGAGAGAG 120
Db 61 TCGACCCCGGTGTCGGGCTAGTCAGAGCGAGCGAGCGCGCGGTGAGAGAGAGAGAG 120

QY 121 CCCGCGATGGAAGCGGTGCGCGACCGGCTGGCGTGGTGAAGAGAGCGCGCGGCGATC 180
Db 121 CCCGCGATGGAAGCGGTGCGCGACCGGCTGGCGTGGTGAAGAGAGCGCGCGGCGATC 180

QY 181 GCGCGGCGGTGCGCGCGGCGGCTGGTCCAGAGGAGCTGAAGAGTGGTGGCGCGCGC 240
Db 181 GCGCGGCGGTGCGCGCGGCGGCTGGTCCAGAGGAGCTGAAGAGTGGTGGCGCGCGC 240

QY 241 ACTGTGGCAACATCGAGAGCTGCTGCTCAAGTGAAGAGTGAAGAGTGAAGAGTGAAG 300
Db 241 ACTGTGGCAACATCGAGAGCTGCTGCTCAAGTGAAGAGTGAAGAGTGAAGAGTGAAG 300

QY 301 TTGATCCCGCTACAGATGTGACCTATCAAAATGAAGAGGACATCTCTCCATGTTCTCAGCT 360
Db 301 TTGATCCCGCTACAGATGTGACCTATCAAAATGAAGAGGACATCTCTCCATGTTCTCAGCT 360

QY 361 ATCCGTTCTCAGACAGCGGTGTAGACATCTGCAATCAAAATGAAGAGTGAAGAGTGAAG 420
Db 361 ATCCGTTCTCAGACAGCGGTGTAGACATCTGCAATCAAAATGAAGAGTGAAGAGTGAAG 420

QY 421 GACACCTGTCTCAGGAGCAGCAGTGGTGGAGGAGCAGTGGTGAAGAGTGAAGAGTGAAG 480
Db 421 GACACCTGTCTCAGGAGCAGCAGTGGTGGAGGAGCAGTGGTGAAGAGTGAAGAGTGAAG 480

QY 481 GCCCTCAGCATCTGCACACCGGAGCGCTACAGTCCATGAAGAGCGGAGTGAAGAGTGAAG 540
Db 481 GCCCTCAGCATCTGCACACCGGAGCGCTACAGTCCATGAAGAGCGGAGTGAAGAGTGAAG 540

QY 541 GGGCAGATCAATTAACATAGATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACC 600
Db 541 GGGCAGATCAATTAACATAGATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACC 600

QY 601 CACTTCTATAGTGCACCAAGTATGCGCTCAGTGGTGAAGAGTGAAGAGTGAAGAGTGAAG 660
Db 601 CACTTCTATAGTGCACCAAGTATGCGCTCAGTGGTGAAGAGTGAAGAGTGAAGAGTGAAG 660

QY 661 CTTGGGAGGCGCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTTGGAGACA 720
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Db 661 CTTGGGAGGCGCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTTGGAGACA 720
QY 721 CAATTGCGCTTCAAACTCCACGACAAAGACCTGAGAGGAGCTGCCACCTATGAGCAA 780
Db 721 CAATTGCGCTTCAAACTCCACGACAAAGACCTGAGAGGAGCTGCCACCTATGAGCAA 780
QY 781 ATGAAGTGTCTCAAAACCGAGGATGTGCGGAGGTGTATCTAGCTCTCAGCACCCCC 840
Db 781 ATGAAGTGTCTCAAAACCGAGGATGTGCGGAGGTGTATCTAGCTCTCAGCACCCCC 840
QY 841 GCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCAGGTGACCTAGTACTG 900
Db 841 GCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCAGGTGACCTAGTACTG 900
QY 901 TGGGAGCTCCTCTTCCCTCCACCCCTTCATGGGTTCCTCTGCTCTCTGATTTTAGG 960
Db 901 TGGGAGCTCCTCTTCCCTCCACCCCTTCATGGGTTCCTCTGCTCTCTGATTTTAGG 960
QY 961 TGTGATTTCTGGATCAGGGATACCACTTCCTGTCCACCCCGACCGAGGCTAGAAA 1020
Db 961 TGTGATTTCTGGATCAGGGATACCACTTCCTGTCCACCCCGACCGAGGCTAGAAA 1020
QY 1021 ATTGTTTGGATTTTATATCATCTTGTCAAAATGCTTCAATGCTTAATGTGAAAAATG 1080
Db 1021 ATTGTTTGGATTTTATATCATCTTGTCAAAATGCTTCAATGCTTAAATGTGAAAAATG 1080
QY 1081 GCGTGGGAAAGAGGTGGTGTCCCTAATGCTTTTACTTTTAACTTCTCTGTCCTCC 1140
Db 1081 GCGTGGGAAAGAGGTGGTGTCCCTAATGCTTTTACTTTTAACTTCTCTGTCCTCC 1140
QY 1141 TGGGCACTTGGCTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGTGTG 1200
Db 1141 TGGGCACTTGGCTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGTGTG 1200
QY 1201 GCCAAATCCCACTTCTTTCGACCTCAACCTCTGTGGCTCAGGGCTGGGGTGGCAGAG 1260
Db 1201 GCCAAATCCCACTTCTTTCGACCTCAACCTCTGTGGCTCAGGGCTGGGGTGGCAGAG 1260
QY 1261 GAGGCTTTCACCTTATATCTGTGTTGTATCCAGGGCTCCAGACTTCTCTCTGCTGC 1320
Db 1261 GAGGCTTTCACCTTATATCTGTGTTGTATCCAGGGCTCCAGACTTCTCTCTGCTGC 1320
QY 1321 CCCTGAGACCTCTCCCTCTTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
Db 1321 CCCTGAGACCTCTCCCTCTTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
QY 1381 TCTTGTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1440
Db 1381 TCTTGTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1440
QY 1441 GGGCTTGGCCAGTGGATTTTCATGGTGTATTTAAAAAGAAAAATCGAACCAAAAAA 1500
Db 1441 GGGCTTGGCCAGTGGATTTTCATGGTGTATTTAAAAAGAAAAATCGAACCAAAAAA 1500
QY 1501 AAAAA 1505
Db 1501 AAAAA 1505

RESULT 3
US-10-201-858-377
; Sequence 377, Application US/10201858
; Publication No. US2004003837A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
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; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P343ORIC464
; CURRENT APPLICATION NUMBER: US/10/201,858
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-201-858-377

Query Match 100.0%; Score 1505; DB 13; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 CGCGGATCGGACCCAAGCAGGTCCGGCGCGGCGCAGAGAGCGCGCGGTTCAGCTCC 60
Db 1 CGCGGATCGGACCCAAGCAGGTCCGGCGCGGCGCAGAGAGCGCGCGGTTCAGCTCC 60

Qy 61 TCGACCCCGCTGTGCGGGTAGTCTCCAGCGAGCGGACGCGCGCGCTGGGCCATGCCAGG 120
Db 61 TCGACCCCGCTGTGCGGGTAGTCTCCAGCGAGCGGACGCGCGCGCTGGGCCATGCCAGG 120

Qy 121 CCCGGCATGAGCGGTCGCGCGACCGGCTGGCGCTGGTGACGGGGGCCCTCGGGGGGCATC 180
Db 121 CCCGGCATGAGCGGTCGCGCGACCGGCTGGCGCTGGTGACGGGGGGCCCTCGGGGGGCATC 180

Qy 181 GGCGGGCGCTGGCGCGGGCCCTGGTCCAGCAGGACCTGAAGGTCGTGGGCTGCGCCCGCG 240
Db 181 GGCGGGCGCTGGCGCGGGCCCTGGTCCAGCAGGACCTGAAGGTCGTGGGCTGCGCCCGCG 240

Qy 241 ACTGTGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAAGCTACCCCGGACT 300
Db 241 ACTGTGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAAGCTACCCCGGACT 300

Qy 301 TTGATCCCTACAGATGTGACCTATCAATGAAGAGGACATCCTCTCCATGTTCACGCT 360
Db 301 TTGATCCCTACAGATGTGACCTATCAATGAAGAGGACATCCTCTCCATGTTCACGCT 360

Qy 361 ATCCGTTCTCAGCAGCGGTGTAGACATCTGCAATCAACAATGTGGCTTGGCCCGGCT 420
Db 361 ATCCGTTCTCAGCAGCGGTGTAGACATCTGCAATCAACAATGTGGCTTGGCCCGGCT 420

Qy 421 GACACCTGCTCTCAGGCGACGACAGTGGTGGAGGACATGTTCAAATGTGAACGTGCTG 480
Db 421 GACACCTGCTCTCAGGCGACGACAGTGGTGGAGGACATGTTCAAATGTGAACGTGCTG 480

Qy 481 GGCCTTCAGCATCTGCACACGCGGAAGCCCTACCAAGTCCATGAAGAGCGGAATGTGGACGAT 540

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Db 1381 TCTTGTCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTTGGCAGCAGAACCA 1440
Qy 1441 GGGCTGGCCCGAGTGGATTTCATGTGTGATCATTAATAAAGAAAAATCAACCAAAAAA 1500
Db 1441 GGGCTGGCCCGAGTGGATTTCATGTGTGATCATTAATAAAGAAAAATCAACCAAAAAA 1500
Qy 1501 AAAAA 1505
Db 1501 AAAAA 1505

RESULT 5
US-10-208-024-377
; Sequence 377, Application US/10208024
; Publication No. US20040048335A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C538
; CURRENT APPLICATION NUMBER: US/10/208,024
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-208-024-377

Query Match 100.0%; Score 1505; DB 13; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGATCGGACCCAAAGCAGGTTCGGCGCGCGCGGAGAGAGCGCGCGGTCTCAGTCC 60
Db 1 CGCGATCGGACCCAAAGCAGGTTCGGCGCGCGCGGAGAGAGCGCGCGGTCTCAGTCC 60
Qy 61 TCGACCCCGCTCGGGCTAGTCCAGCGAGCGGAGCGCGCGGTGGGCCCATGGCCAGG 120
Db 61 TCGACCCCGCTCGGGCTAGTCCAGCGAGCGGAGCGCGCGGTGGGCCCATGGCCAGG 120
Qy 121 CCCGGCATGGAGCGGTGGCGCGACCGGCTGGCGCTGGTACCGGGGGCCTCGGGGGGCATC 180
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Db 121 CCCGGCATGGAGCGGTGGCGCGACCGGCTGGCTGGTGA CGGGGGCCTCGGGGGGCATC 180
Qy 181 GGC CGGCGCTGGCCCGGGCCCTGGTCCAGCAGGAGCTGAAGGTGGTGGGCTGGCCCGC 240
Db 181 GGC CGGCGCTGGCCCGGGCCCTGGTCCAGCAGGAGCTGAAGGTGGTGGGCTGGCCCGC 240
Qy 241 ACTGTGGGCAACATCGAGGAGCTGGCTGCTCAATGTAAGAGTGCAGGCTACCCCGGACT 300
Db 241 ACTGTGGGCAACATCGAGGAGCTGGCTGCTCAATGTAAGAGTGCAGGCTACCCCGGACT 300
Qy 301 TTGATCCCTACAGATGTGACCTATCAAAATGAAGAGGACATCCCTCTCCATGTTCTCAGCT 360
Db 301 TTGATCCCTACAGATGTGACCTATCAAAATGAAGAGGACATCCCTCTCAATGTTCTCAGCT 360
Qy 361 ATCGGTTCTCAGCAGCGGTGTAGACATCTGCAATCAATGCTGGCTTGGCCCGGGCT 420
Db 361 ATCGGTTCTCAGCAGCGGTGTAGACATCTGCAATCAATGCTGGCTTGGCCCGGGCT 420
Qy 421 GACACCTGCTCTCAGGCAGCACCGAGTGGTGGAGGACATGTTCAATGTGAACGTGTG 480
Db 421 GACACCTGCTCTCAGGCAGCACCGAGTGGTGGAGGACATGTTCAATGTGAACGTGTG 480
Qy 481 GCCCTCAGCATCTGCACACGGGAAGCCTTACCAGTCCATGAAGAGCGGAATGTGACGAT 540
Db 481 GCCCTCAGCATCTGCACACGGGAAGCCTTACCAGTCCATGAAGAGCGGAATGTGACGAT 540
Qy 541 GGGCAGCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACC 600
Db 541 GGGCAGCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACC 600
Qy 601 CACTTCTATAGTGGCCACCAAGTATGCCGTCTACTGGCTGACAGAGGGACTCAGGCAAGAG 660
Db 601 CACTTCTATAGTGGCCACCAAGTATGCCGTCTACTGGCTGACAGAGGGACTCAGGCAAGAG 660
Qy 661 CTTGGGAGGCCCCAGACCCACATCCGAGCCACGTGCACTCTCCAGGTGTGGTGAGACA 720
Db 661 CTTGGGAGGCCCCAGACCCACATCCGAGCCACGTGCACTCTCCAGGTGTGGTGAGACA 720
Qy 721 CAATTCGGCTTCAAACTCCAGACAGGACCCCTGAGAAAGGAGCTGCCACCTATGAGCAA 780
Db 721 CAATTCGGCTTCAAACTCCAGACAGGACCCCTGAGAAAGGAGCTGCCACCTATGAGCAA 780
Qy 781 ATGAAGTGTCTCAAACTCCAGAGGATGTGCCGAGGCTGTATCTAGCTCTCAGCACCCCC 840
Db 781 ATGAAGTGTCTCAAACTCCAGAGGATGTGCCGAGGCTGTATCTAGCTCTCAGCACCCCC 840
Qy 841 GCACATCCAGATTGGAGACATCCAGATGAGGCCCCACGGAGCAGGTGACCTAGTGACTG 900
Db 841 GCACATCCAGATTGGAGACATCCAGATGAGGCCCCACGGAGCAGGTGACCTAGTGACTG 900
Qy 901 TGGGAGCTCTCTTCCCTCCACCCCTTCATGGCTTGCCTTGCCTCTGGATTTTAGG 960
Db 901 TGGGAGCTCTCTTCCCTCCACCCCTTCATGGCTTGCCTTGCCTCTGGATTTTAGG 960
Qy 961 TGTGATTTCTGGATCAGGGATACCACTCTCTGTCCACACCCCGACAGGGGCTAGAAA 1020
Db 961 TGTGATTTCTGGATCAGGGATACCACTCTCTGTCCACACCCCGACAGGGGCTAGAAA 1020
Qy 1021 ATTTGTTTGGATTTTATATCATCTTCTCAAAATGCTTCAGTTGTAATGTGAAAAATG 1080
Db 1021 ATTTGTTTGGATTTTATATCATCTTCTCAAAATGCTTCAGTTGTAATGTGAAAAATG 1080
Qy 1081 GGCTGGGAAAGAGGTGGTGTCCCTTAATGTTTACTTGTACTTGTCTTCTTGTGCCCC 1140
Db 1081 GGCTGGGAAAGAGGTGGTGTCCCTTAATGTTTACTTGTACTTGTCTTCTTGTGCCCC 1140
Qy 1141 TGGGCACATTGGCCTTTGTCTGCTCTCAGTGTCTTCCCTTTCACATGGGAAAGAGTTGTG 1200
Db 1141 TGGGCACATTGGCCTTTGTCTGCTCTCAGTGTCTTCCCTTTCACATGGGAAAGAGTTGTG 1200
Qy 1201 GCCAAAATCCCGCATCTTCTTTCGACCTCAACGTCTGTGGCTCAGGGCTGGGGGTGGCAGAG 1260
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Db 1021 ATTTGTTTGAGATTTTATATCATCTTGTCAAATTTGCTTCAATGTAATAATG 1080
Qy 1081 GGCTGGGGAAGAGGTGGTCCCTAATGTTTAACTTGTAACTTGTGGCCCC 1140
Db 1081 GGCTGGGGAAGAGGTGGTCCCTAATGTTTAACTTGTAACTTGTGGCCCC 1140
Qy 1141 TGGGCACTTGGCCTTTGCTGCTCTCAGTGTCTTCCCTTGACATGGGAAGGAGTTGTG 1200
Db 1141 TGGGCACTTGGCCTTTGCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAGGAGTTGTG 1200
Qy 1201 GCCAAATCCCACTCTTCTGACCTCAACCTGCTGTGGCTCAGGGCTGGGTCAGAGG 1260
Db 1201 GCCAAATCCCACTCTTCTGACCTCAACCTGCTGTGGCTCAGGGCTGGGTCAGAGG 1260
Qy 1261 GAGGCTTCACTTATATCTGTGTTTATCCAGGGCTCCAGATTCCTCTCTGCTGTC 1320
Db 1261 GAGGCTTCACTTATATCTGTGTTTATCCAGGGCTCCAGATTCCTCTCTGCTGTC 1320
Qy 1321 CCCAGTCACTCTCCCTTATCTATCTCTCTGCTCCAGCCAGCTTGTGCT 1380
Db 1321 CCCAGTCACTCTCTCCCTTATCTATCTCTCTGCTCCAGCCAGCTTGTGCT 1380
Qy 1381 TCTTCTCCCTCTGGGCTATCCCTCCACTCTGACTCTGACTATGGCAGCAACCA 1440
Db 1381 TCTTCTCCCTCTGGGCTATCCCTCCACTCTGACTCTGACTATGGCAGCAACCA 1440
Qy 1441 GGGCTGGCCAGTGGATTCATGTGATCAATAAAGAAAAATCGAACCAAAAA 1500
Db 1441 GGGCTGGCCAGTGGATTCATGTGATCAATAAAGAAAAATCGAACCAAAAA 1500
Qy 1501 AAAAA 1505
Db 1501 AAAAA 1505

RESULT 7

US-10-063-745-127
; Sequence 127, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 127
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-745-127

Query Match 100.0%; Score 1505; DB 13; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGGATCGGACCAAGCAGGTGGCGGGCGGCGGAGGAGCGCGGCGGTCACTCC 60
Db 1 CGGGATCGGACCAAGCAGGTGGCGGGCGGCGGAGGAGCGCGGCGGTCACTCC 60
Qy 61 TCGACCCCGTGTGGGCTAGTCCAGCGAGCGGAGCGGGCGGCGGTGGCCAGG 120
Db 61 TCGACCCCGTGTGGGCTAGTCCAGCGAGCGGAGCGGGCGGCGGTGGCCAGG 120

Qy 121 CCCGSCATGGAGCGTGGCGGACCGGCTGGCGCTGGTGAAGGGGGCTTCGGGGGGCATC 180
Db 121 CCCGSCATGGAGCGTGGCGGACCGGCTGGCGCTGGTGAAGGGGGCTTCGGGGGGCATC 180
Qy 181 GGGCGGGCGGTGGGGCCCGGGCCCTGGTCCAGCAGGAGCTGAAGGTGGGGCTGGCCCGC 240
Db 181 GGGCGGGCGGTGGGGCCCGGGCCCTGGTCCAGCAGGAGCTGAAGGTGGGGCTGGCCCGC 240
Qy 241 ACTGTGGGAACATCGAGGAGCTGGCTGCTCAATGTAAGTGCAGGCTACCCCGGACT 300
Db 241 ACTGTGGGAACATCGAGGAGCTGGCTGCTCAATGTAAGTGCAGGCTACCCCGGACT 300
Qy 301 TTGATCCCTACAGATGTACCTATCAAAATGAAGAGGACATCCCTCTCCATGTTCTCAGCT 360
Db 301 TTGATCCCTACAGATGTACCTATCAAAATGAAGAGGACATCCCTCTCCATGTTCTCAGCT 360
Qy 361 ATCCGTTCTCAGCAGCGGTGTAGACATCTGGAATCAACATGCTGGCTTGGCCCGGCT 420
Db 361 ATCCGTTCTCAGCAGCGGTGTAGACATCTGGAATCAACATGCTGGCTTGGCCCGGCT 420
Qy 421 GACACCTGCTCTCAGGAGCAGCAGTGGTGGAGGACATGTTCAATGTCAACGTGTG 480
Db 421 GACACCTGCTCTCAGGAGCAGCAGTGGTGGAGGACATGTTCAATGTCAACGTGTG 480
Qy 481 GCCCTCAGCATCTGCACACGGGAAGCCTACCAAGTCCATGAAGGAGCGGAATGTGGACAT 540
Db 481 GCCCTCAGCATCTGCACACGGGAAGCCTACCAAGTCCATGAAGGAGCGGAATGTGGACAT 540
Qy 541 GGGCACATCAATTAACATCAATAGCATGCTGGCCACCGAGTGTACCCCTGTCTGACC 600
Db 541 GGGCACATCAATTAACATCAATAGCATGCTGGCCACCGAGTGTACCCCTGTCTGACC 600
Qy 601 CACTTCTATAGTCCACCAAGTATGCGCTCACTGCTGACAGAGGAGCTAGGCAAGAG 660
Db 601 CACTTCTATAGTCCACCAAGTATGCGCTCACTGCTGACAGAGGAGCTAGGCAAGAG 660
Qy 661 CTTGGGAGGCGCCAGACCCACATCCGAGCCAGTCACTCTCCAGGTGTGGTGAGACA 720
Db 661 CTTGGGAGGCGCCAGACCCACATCCGAGCCAGTCACTCTCCAGGTGTGGTGAGACA 720
Qy 721 CAATTCGCTTCAAACTCCACAGAACCCCTGAGAGGAGCTGCCACCTATGAGCAA 780
Db 721 CAATTCGCTTCAAACTCCACAGAACCCCTGAGAGGAGCTGCCACCTATGAGCAA 780
Qy 781 ATGAAGTGTCTCAAAACCCGAGGATGTGCGGAGGCTGTTATCTACGTCTCAGCACCC 840
Db 781 ATGAAGTGTCTCAAAACCCGAGGATGTGCGGAGGCTGTTATCTACGTCTCAGCACCC 840
Qy 841 GCACACATCCAGATTGGAGACATCCAGATGAGGCGCCACGGAGCAGGTGACCTAGTACTG 900
Db 841 GCACACATCCAGATTGGAGACATCCAGATGAGGCGCCACGGAGCAGGTGACCTAGTACTG 900
Qy 901 TGGGAGCTCCTCTTCCCTCCCACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 TGGGAGCTCCTCTTCCCTCCCACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Qy 961 TGTGATTTCTGATCAGCGGATACCACTTCTGCTCCACACCCCGAGGAGGCTAGAAA 1020
Db 961 TGTGATTTCTGATCAGCGGATACCACTTCTGCTCCACACCCCGAGGAGGCTAGAAA 1020
Qy 1021 ATTTGTTTGAGATTTTATATCATCTTGTCAAATTTGCTTCAATGTAATAATG 1080
Db 1021 ATTTGTTTGAGATTTTATATCATCTTGTCAAATTTGCTTCAATGTAATAATG 1080
Qy 1081 GGTGGGGAAGAGGTGGTGGCTTCAATGTTTAACTTGTAACTTGTCTGCTGCTGCTGCTG 1140
Db 1081 GGTGGGGAAGAGGTGGTGGCTTCAATGTTTAACTTGTAACTTGTCTGCTGCTGCTGCTG 1140
Qy 1141 TGGGCACTTGGCCTTTGCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAGGAGTTGTG 1200
Db 1141 TGGGCACTTGGCCTTTGCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAGGAGTTGTG 1200

```
QY 1201 GCCAAATCCCATCTTCTTGACCTCAACGCTGTGGCTCAGGCTGGGTGGCAGAGG 1260
Db 1201 GCCAAATCCCATCTTCTTGACCTCAACGCTGTGGCTCAGGCTGGGTGGCAGAGG 1260
QY 1261 GAGGCTTCACTTATATCTGTGTGTTATCCAGGCTCCAGACTTCTCTCTGCTGC 1320
Db 1261 GAGGCTTCACTTATATCTGTGTGTTATCCAGGCTCCAGACTTCTCTCTGCTGC 1320
QY 1321 CCCACTGACCTCTCCCTTATCTATCTCTCTCTGCTCCAGCTCCAGCTTGGCT 1380
Db 1321 CCCACTGACCTCTCCCTTATCTATCTCTCTCTGCTCCAGCTCCAGCTTGGCT 1380
QY 1381 TCTTGTCCCTCTCTGGGCTCATCTCCCTCCACTCTGACTCTGACTATGGCAGCAGAACCA 1440
Db 1381 TCTTGTCCCTCTCTGGGCTCATCTCCCTCCACTCTGACTCTGACTATGGCAGCAGAACCA 1440
QY 1441 GGGCTTGGCCCACTGATTTGATGATCATTTAAAAAGAAAAATCGCAACCAAAAAA 1500
Db 1441 GGGCTTGGCCCACTGATTTGATGATCATTTAAAAAGAAAAATCGCAACCAAAAAA 1500
QY 1501 AAAAA 1505
Db 1501 AAAAA 1505

RESULT 8
US-10-063-512-127
; Sequence 127, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 127
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-512-127

Query Match 100.0%; Score 1505; DB 13; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGATCGGACCCAGCAGTCTCGCGCGCGGCGGAGAGCGGCGGCGTCACTCC 60
Db 1 CGCGGATCGGACCCAGCAGTCTCGCGCGGCGGAGAGCGGCGGCGTCACTCC 60
QY 61 TCGACCCCGGTGTGGGCTAGTCTCAGCGAGCGGCGGCGGCGTGGGCCCATGCCAGG 120
Db 61 TCGACCCCGGTGTGGGCTAGTCTCAGCGAGCGGCGGCGGCGTGGGCCCATGCCAGG 120
QY 121 CCCGCGATGGACGGTGTGCGGACCGGCTGCGTGTGACGGGGCGCTCGGGGGGCATC 180
Db 121 CCCGCGATGGACGGTGTGCGGACCGGCTGCGTGTGACGGGGCGCTCGGGGGGCATC 180
QY 181 GCGCGGCGGCTGGCCCGGCGCTTGTTCAGCAGGAGCTGAAGGTGTGGGCTGCGCGCG 240
Db 181 GCGCGGCGGCTGGCCCGGCGCTTGTTCAGCAGGAGCTGAAGGTGTGGGCTGCGCGCG 240
QY 241 ACTGTGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGGCTACCCCGGACT 300
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Db 241 ACTGTGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGGCTACCCCGGACT 300
QY 301 TTGATCCCCCTCAGATGTGACCTATCAAAATGAAGAGGACATCTCTCCATGTTCTCAGCT 360
Db 301 TTGATCCCCCTCAGATGTGACCTATCAAAATGAAGAGGACATCTCTCCATGTTCTCAGCT 360
QY 361 ATCCCTTCTCAGCAGCGGCTGTAGCATCTGCATCAACAATGCTGGTGTGCCCGGCT 420
Db 361 ATCCCTTCTCAGCAGCGGCTGTAGCATCTGCATCAACAATGCTGGTGTGCCCGGCT 420
QY 421 GACACCCCTGCTCTCAGGCGAGCAGCTGTGGTGAAGGACATGTTCAATGTGAACGTGTG 480
Db 421 GACACCCCTGCTCTCAGGCGAGCAGCTGTGGTGAAGGACATGTTCAATGTGAACGTGTG 480
QY 481 GCCCTCAGCATCTGCACACGCGGAAGCTTACCATGAGGAGCGGAATGTGACCAT 540
Db 481 GCCCTCAGCATCTGCACACGCGGAAGCTTACCATGAGGAGCGGAATGTGACCAT 540
QY 541 GGGCAGCATTTAATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACC 600
Db 541 GGGCAGCATTTAATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACC 600
QY 601 CACTTCTATAGTGCACCAAGTATGCGCTCACTCGCTGACAGAGGAGTGCAGGCAAGAG 660
Db 601 CACTTCTATAGTGCACCAAGTATGCGCTCACTCGCTGACAGAGGAGTGCAGGCAAGAG 660
QY 661 CTTGGGAGGCCAGACCCACATCCGAGCCACGTCATCTCTCCAGGTGTGGTGAGACA 720
Db 661 CTTGGGAGGCCAGACCCACATCCGAGCCACGTCATCTCTCCAGGTGTGGTGAGACA 720
QY 721 CAATTGCGCTTCAAACTCCAGCAAGGACCCCTGAGAGGAGCTGCCACCTATGAGCAA 780
Db 721 CAATTGCGCTTCAAACTCCAGCAAGGACCCCTGAGAGGAGCTGCCACCTATGAGCAA 780
QY 781 ATGAAGTGTCTCAAAACCGGAGTGTGGCCAGGCTGTATCTAGCTCCTCAGCACCCCC 840
Db 781 ATGAAGTGTCTCAAAACCGGAGTGTGGCCAGGCTGTATCTAGCTCCTCAGCACCCCC 840
QY 841 GCACATATCCAGATTGGAGACATCCAGATGAGGCGCCAGGAGGAGTGCACCTAGTACTG 900
Db 841 GCACATATCCAGATTGGAGACATCCAGATGAGGCGCCAGGAGGAGTGCACCTAGTACTG 900
QY 901 TGGAGCTCTCTCTCCCTCCCAACCTTCAATGCTGTGCTCTCTCTCTGCTCTGCTTTAGG 960
Db 901 TGGAGCTCTCTCTCCCTCCCAACCTTCAATGCTGTGCTCTCTCTCTGCTCTGCTTTAGG 960
QY 961 TGTGATTTCTGGATCAGGAGTACCACTTCTCTCCACACCCCGACCCAGGCGGTAGAAA 1020
Db 961 TGTGATTTCTGGATCAGGAGTACCACTTCTCTCCACACCCCGACCCAGGCGGTAGAAA 1020
QY 1021 ATTTGTTTGTAGATTTTATATCATCTTGTCAAAATGCTTCAAGTTGTAATGTGAAAAATG 1080
Db 1021 ATTTGTTTGTAGATTTTATATCATCTTGTCAAAATGCTTCAAGTTGTAATGTGAAAAATG 1080
QY 1081 GGCTGGGGAAGAGGAGTGTGCTCCCTAAATGTTTTTACTTTTAACTTTTCTTTGTCCTCC 1140
Db 1081 GGCTGGGGAAGAGGAGTGTGCTCCCTAAATGTTTTTACTTTTAACTTTTCTTTGTCCTCC 1140
QY 1141 TGGGCACTTGGCCCTTCTGCTCTCAGTGTCTTCCCTTTTGCATGAGGAAAGAGTGTG 1200
Db 1141 TGGGCACTTGGCCCTTCTGCTCTCAGTGTCTTCCCTTTTGCATGAGGAAAGAGTGTG 1200
QY 1201 GCCAAAAATCCCATCTTCTTGTGCACTCAAGCTGTGTGGCTCAGGGCTGGGGTGGCAGAGG 1260
Db 1201 GCCAAAAATCCCATCTTCTTGTGCACTCAAGCTGTGTGGCTCAGGGCTGGGGTGGCAGAGG 1260
QY 1261 GAGGCTTCACTTATATCTGTGTGTTATCCAGGCTCCAGACTTCCCTCTCTGCTGCTC 1320
Db 1261 GAGGCTTCACTTATATCTGTGTGTTATCCAGGCTCCAGACTTCCCTCTCTGCTGCTC 1320
QY 1321 CCCACTGACCTCTCCCTTATCTATCTCTCTGCTTCCAGCTCCCGGCTACCCCGGACT 1380
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Db 1321 CCACCTGCACCTCTCCCTTATCTATCTCTCTCTCGGCTCCCGAGCCAGCTCTGGCT 1380
Qy 1381 TCTGTCCCTCTCGGGGTCACTCCCTCACTCTGACTCTGACTATGGCAGGAGAACCA 1440
Db 1381 TCTGTCCCTCTCGGGGTCACTCCCTCACTCTGACTCTGACTATGGCAGGAGAACCA 1440
Qy 1441 GGGCTGGCCAGTGGATTTTCATGTGATCATTAAGAAAGAAATCCACCAAAAAA 1500
Db 1441 GGGCTGGCCAGTGGATTTTCATGTGATCATTAAGAAAGAAATCCACCAAAAAA 1500
Qy 1501 AAAAA 1505
Db 1501 AAAAA 1505

RESULT 9
US-10-063-513-127
; Sequence 127, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 127
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-513-127

Query Match 100.0%; Score 1505; DB 13; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGGATCGGACCCCAAGCAGGTTCGGCGCGCGGCGGAGAGAGCGCGCGGTTCAGCTCC 60
Db 1 CGCGGATCGGACCCCAAGCAGGTTCGGCGCGCGGCGGAGAGAGCGCGCGGTTCAGCTCC 60
Qy 61 TCGACCCCGGTTCGGGTAGTTCAGCGAGGCGGAGCGGCGCGGTTCAGCTCCATGGCCAGG 120
Db 61 TCGACCCCGGTTCGGGTAGTTCAGCGAGGCGGAGCGGCGCGGTTCAGCTCCATGGCCAGG 120
Qy 121 CCGGCGATGAGCGGTTCGGCGCGGCGGCGGTTCAGCGGCGGCGGTTCAGCGGCGGCGATC 180
Db 121 CCGGCGATGAGCGGTTCGGCGCGGCGGCGGTTCAGCGGCGGCGGTTCAGCGGCGGCGATC 180
Qy 181 GCGCGGCGGTTCGGCGCGGCGGCGGTTCAGCGGCGGCGGTTCAGCGGCGGCGGTTCAGCG 240
Db 181 GCGCGGCGGTTCGGCGCGGCGGCGGTTCAGCGGCGGCGGTTCAGCGGCGGCGGTTCAGCG 240
Qy 241 ACTGTGGGCAACATCGAGAGCTGGCTGCTGAAATGAAGAGGACATCTCTCCATGTTCTCAGCT 300
Db 241 ACTGTGGGCAACATCGAGAGCTGGCTGCTGAAATGAAGAGGACATCTCTCCATGTTCTCAGCT 300
Qy 301 TTGATCCCCCTACAGATGTGACCTTATCAAAATGAAGAGGACATCTCTCCATGTTCTCAGCT 360
Db 301 TTGATCCCCCTACAGATGTGACCTTATCAAAATGAAGAGGACATCTCTCCATGTTCTCAGCT 360
Qy 361 ATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTGGCCCGGCT 420
Db 361 ATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTGGCCCGGCT 420
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Qy 421 GACACCTCTCTCAGGAGCACACAGTGGTTGGAGGACATGTTCAATGTGAACGTGCTG 480
Db 421 GACACCTCTCTCAGGAGCACACAGTGGTTGGAGGACATGTTCAATGTGAACGTGCTG 480
Qy 481 GCCCTCAGCATCTGCACACGGGAAGCCTTACAGTCCCATGAAGGAGCGGAATGTGGACAT 540
Db 481 GCCCTCAGCATCTGCACACGGGAAGCCTTACAGTCCCATGAAGGAGCGGAATGTGGACAT 540
Qy 541 GGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTCTCTGTGACC 600
Db 541 GGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTCTCTGTGACC 600
Qy 601 CACTTCTATAGTGCACCAAGTATGCCGTCACTGCGTGCAGAGGAGCTCAGGCAAGAG 660
Db 601 CACTTCTATAGTGCACCAAGTATGCCGTCACTGCGTGCAGAGGAGCTCAGGCAAGAG 660
Qy 661 CTTGGGAGGCGCCAGACCCACATCCGAGCCAGCTGTATCTCTCCAGGTGTGGTGGAGACA 720
Db 661 CTTGGGAGGCGCCAGACCCACATCCGAGCCAGCTGTATCTCTCCAGGTGTGGTGGAGACA 720
Qy 721 CAATTCGCTTCAAACTCCAGCAAGACCCCTGAGAAGGAGCTGCCACCTATGAGCAA 780
Db 721 CAATTCGCTTCAAACTCCAGCAAGACCCCTGAGAAGGAGCTGCCACCTATGAGCAA 780
Qy 781 ATGAAGTGTCTCAAAACCGAGGATGTGGCGGAGGCTGTATCTACGTCTCTCAGCACCCCC 840
Db 781 ATGAAGTGTCTCAAAACCGAGGATGTGGCGGAGGCTGTATCTACGTCTCTCAGCACCCCC 840
Qy 841 GCACACATCCAGATTTGGAGACATCCAGATGAGGCGCCACGAGAGCTGACCTAGTGACTG 900
Db 841 GCACACATCCAGATTTGGAGACATCCAGATGAGGCGCCACGAGAGCTGACCTAGTGACTG 900
Qy 901 TGGGAGCTCTCTCTCCCTCCACCTTCATGGCTTCGCTTCGCTCTGATTTTAGG 960
Db 901 TGGGAGCTCTCTCTCCCTCCACCTTCATGGCTTCGCTTCGCTCTGATTTTAGG 960
Qy 961 TGTGATTTCTGGATCAGGGATACCACTTCTCTGCCACACCCACGAGGGGCTAGAAA 1020
Db 961 TGTGATTTCTGGATCAGGGATACCACTTCTCTGCCACACCCACGAGGGGCTAGAAA 1020
Qy 1021 ATTTGTTTGAGATTTTATATCATCTTCTCAAAATGCTTCAATGTAATGTGAAAAATG 1080
Db 1021 ATTTGTTTGAGATTTTATATCATCTTCTCAAAATGCTTCAATGTAATGTGAAAAATG 1080
Qy 1081 GGTCTGGGAAAGAGGAGTGTCCCTAATGTTTACTGTTTAACTGTTCTTGTGCCCC 1140
Db 1081 GGTCTGGGAAAGAGGAGTGTCCCTAATGTTTACTTGTGTTAACTTGTCTTGTGCCCC 1140
Qy 1141 TGGGCACCTTGGCTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGTGTG 1200
Db 1141 TGGGCACCTTGGCTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGTGTG 1200
Qy 1201 GCAAAATCCCATCTTCTTGACCTCAACGCTCTGTGGCTCAGGCTGGGGTGGCAGAG 1260
Db 1201 GCAAAATCCCATCTTCTTGACCTCAACGCTCTGTGGCTCAGGCTGGGGTGGCAGAG 1260
Qy 1261 GAGGCTTCACTTATATCTGTTGTTATCCAGGCTCCAGACTTCTCTCTGCTGCTG 1320
Db 1261 GAGGCTTCACTTATATCTGTTGTTATCCAGGCTCCAGACTTCTCTCTGCTGCTG 1320
Qy 1321 CCACCTGCACCCCTCTCCCTCTTATCTATCTCTCTCGGCTCCCGAGCCAGCTCTTGGCT 1380
Db 1321 CCACCTGCACCCCTCTCCCTCTTATCTATCTCTCTCGGCTCCCGAGCCAGCTCTTGGCT 1380
Qy 1381 TCTGTGCCCTCTCGGGGTCACTCCCTCACTCTGACTCTGACTATGGCAGGAGAACCA 1440
Db 1381 TCTGTGCCCTCTCGGGGTCACTCCCTCACTCTGACTCTGACTATGGCAGGAGAACCA 1440
Qy 1441 GGGCGTGGCCAGTGGATTTTCATGTGATCATTAAGAAAGAAATCCGCAACCAAAAAA 1500
Db 1441 GGGCGTGGCCAGTGGATTTTCATGTGATCATTAAGAAAGAAATCCGCAACCAAAAAA 1500
```

QY 1501 AAAAA 1505
 Db 1501 AAAAA 1505

RESULT 10
 US-10-063-569-127
 ; Sequence 127, Application US/10063569
 ; Publication No. US20030018168A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,569
 ; CURRENT FILING DATE: 2002-05-02
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 127
 ; LENGTH: 1505
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-063-569-127

Query Match 100.0%; Score 1505; DB 13; Length 1505;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGATCGGACCAAGCAGGTGCGCGCGCGGCGGAGAGCGCGGGCGTCAGTCC 60
 Db 1 CGCGGATCGGACCAAGCAGGTGCGCGCGCGGCGGAGAGCGCGGGCGTCAGTCC 60

QY 61 TCGACCCCGGTGTCGGGCTAGTCCAGCGAGCGGCGGCGGCGGCGGCGGCGGCGG 120
 Db 61 TCGACCCCGGTGTCGGGCTAGTCCAGCGAGCGGCGGCGGCGGCGGCGGCGGCGG 120

QY 121 CCCGGATGAGCGGTGCGCGGACCGGCTGCGGCTGCGGCGGCGGCGGCGGCGGCGG 180
 Db 121 CCCGGATGAGCGGTGCGCGGACCGGCTGCGGCTGCGGCGGCGGCGGCGGCGGCGG 180

QY 181 GCGCGCGCGGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
 Db 181 GCGCGCGCGGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240

QY 241 ACTGTGGGCAACATCGAGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 Db 241 ACTGTGGGCAACATCGAGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

QY 301 TTGATCCCTACAGATGACATCAATCAATGAAGAGACATCCCTCTCCATGTTCTCAGCT 360
 Db 301 TTGATCCCTACAGATGACATCAATCAATGAAGAGACATCCCTCTCCATGTTCTCAGCT 360

QY 361 ATCCGTTCTCAGCAGCGGTGTAGACATCTGCAATCAACATGCTGCGGCGGCGGCGGCGG 420
 Db 361 ATCCGTTCTCAGCAGCGGTGTAGACATCTGCAATCAACATGCTGCGGCGGCGGCGGCGG 420

QY 421 GACACCTGCTCTCAGGCGAGCACCGAGTGGTGGAGGACATGTTCAATGTGAACGTGCTG 480
 Db 421 GACACCTGCTCTCAGGCGAGCACCGAGTGGTGGAGGACATGTTCAATGTGAACGTGCTG 480

QY 481 GCCCTCAGCATCTGCACACGGAAGCCCTACAGTCCATGAAGAGCGGAATGTGGACGAT 540
 Db 481 GCCCTCAGCATCTGCACACGGAAGCCCTACAGTCCATGAAGAGCGGAATGTGGACGAT 540

QY 541 GGGCACATCAATCAATAGCATGTCTGCGCCACCGAGTGTACCCCTGTCTGTGACC 600

Db 541 GGGCACATCAATCAATAGCATGTCTGCGCCACCGAGTGTACCCCTGTCTGTGACC 600
 QY 601 CACTTCTATAGTGCACCAAGTATGCCGTCACTCGCTGACAGAGGAGTCAAGCAAGAG 660
 Db 601 CACTTCTATAGTGCACCAAGTATGCCGTCACTCGCTGACAGAGGAGTCAAGCAAGAG 660
 QY 661 CTTGGGAGGCCAGACCCACATCCGAGCCACGTGCACTCTCCAGGTGTGGTGGAGACA 720
 Db 661 CTTGGGAGGCCAGACCCACATCCGAGCCACGTGCACTCTCCAGGTGTGGTGGAGACA 720
 QY 721 CAATTGCGCTTCAAACCTCCAGCAAGAGCCCTGAGAAGGAGCTGCCACCTATGAGCAA 780
 Db 721 CAATTGCGCTTCAAACCTCCAGCAAGAGCCCTGAGAAGGAGCTGCCACCTATGAGCAA 780
 QY 781 ATGAAGTGTCTCAAACCCGAGGATGTGCGCGAGGCTGTATCTACGTCTCAGCACCCCC 840
 Db 781 ATGAAGTGTCTCAAACCCGAGGATGTGCGCGAGGCTGTATCTACGTCTCAGCACCCCC 840
 QY 841 GCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCGAGTGAATGACTG 900
 Db 841 GCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCGAGTGAATGACTG 900
 QY 901 TGGGAGCTCTCTCCCTCCCAACCTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 Db 901 TGGGAGCTCTCTCCCTCCCAACCTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 QY 961 TGTGATTTCTGGATCACGGGATACCACTTCTCTGTCACACCCCGAGGCGTAGAAA 1020
 Db 961 TGTGATTTCTGGATCACGGGATACCACTTCTCTGTCACACCCCGAGGCGTAGAAA 1020
 QY 1021 ATTTGTTGAGATTTTATATCATCTTGTCAAATGCTTCAATGTTGTAATGTAATAATG 1080
 Db 1021 ATTTGTTGAGATTTTATATCATCTTGTCAAATGCTTCAATGTTGTAATGTAATAATG 1080
 QY 1081 GGCTGGGGAAGAGGAGTGGTCCCTAAATGTTTACTTGTAACTTGTAACTTGTAACTTGT 1140
 Db 1081 GGCTGGGGAAGAGGAGTGGTCCCTAAATGTTTACTTGTAACTTGTAACTTGTAACTTGT 1140
 QY 1141 TGGGCACTTGGCCCTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAGAGTGTG 1200
 Db 1141 TGGGCACTTGGCCCTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAGAGTGTG 1200
 QY 1201 GCACAAATCCCATCTTCTTGGACCTCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
 Db 1201 GCACAAATCCCATCTTCTTGGACCTCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
 QY 1261 GAGGCTTTCACCTTATATCTGTTTATCCAGGCTTCCAGACTTCTCTCTCTGCTGCTG 1320
 Db 1261 GAGGCTTTCACCTTATATCTGTTTATCCAGGCTTCCAGACTTCTCTCTCTGCTGCTG 1320
 QY 1321 CCCACTGACCCCTCTCCCTCTTATCTATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 Db 1321 CCCACTGACCCCTCTCCCTCTTATCTATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 QY 1381 TCTTGTCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
 Db 1381 TCTTGTCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
 QY 1441 GGGGCTGGCCAGTGGATTTTCAATGTTGATCAATTAATAAAGAAAAATCGCAACCAAAAA 1500
 Db 1441 GGGGCTGGCCAGTGGATTTTCAATGTTGATCAATTAATAAAGAAAAATCGCAACCAAAAA 1500
 QY 1501 AAAAA 1505
 Db 1501 AAAAA 1505

RESULT 11
 US-10-063-551-127
 ; Sequence 127, Application US/10063551
 ; Publication No. US2002018349A1
 ; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 127
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-551-127

Query Match 100.0%; Score 1505; DB 13; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CGCGGATCGGACCAAGCAGGTCCGGCGCGGCGGCGGAGGAGCGCGGGGGCTCAGCTCC	60
Db	1	CGCGGATCGGACCAAGCAGGTCCGGCGCGGCGGCGGAGGAGCGCGGGGGCTCAGCTCC	60
Qy	61	TCGACCCCGGTGTCGGGTAGTCCAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	120
Db	61	TCGACCCCGGTGTCGGGTAGTCCAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	120
Qy	121	CCCGGATGAGCGGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	180
Db	121	CCCGGATGAGCGGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	180
Qy	181	GGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	240
Db	181	GGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	240
Qy	241	ACTGTGGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTGAGGAGTACCCCGGAGCT	300
Db	241	ACTGTGGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTGAGGAGTACCCCGGAGCT	300
Qy	301	TTGATCCCGCTACAGATGAGCTATCAATGAAGAGGACATCCCTCTCAATGTTCTCAGCT	360
Db	301	TTGATCCCGCTACAGATGAGCTATCAATGAAGAGGACATCCCTCTCAATGTTCTCAGCT	360
Qy	361	ATCCGTTCTCAGCAGCGGTGAGACATCTGCATCAACATGCTGGGCTGGCGCGGCT	420
Db	361	ATCCGTTCTCAGCAGCGGTGAGACATCTGCATCAACATGCTGGGCTGGCGCGGCT	420
Qy	421	GACACCTGCTCTCAGGAGCAGCAGTGGTGGAGGACATGTTCAATGTGAAAGCTGCTG	480
Db	421	GACACCTGCTCTCAGGAGCAGCAGTGGTGGAGGACATGTTCAATGTGAAAGCTGCTG	480
Qy	481	GCCCTCAGCTCTGACACCGGAGCGCTTACAGTCCATGAAGAGGCGGAAATGTGAGCAT	540
Db	481	GCCCTCAGCTCTGACACCGGAGCGCTTACAGTCCATGAAGAGGCGGAAATGTGAGCAT	540
Qy	541	GGGACATCATTAACATCAATAGATGCTGGCGCACCGAGGTTACCCCTCTGTGACG	600
Db	541	GGGACATCATTAACATCAATAGATGCTGGCGCACCGAGGTTACCCCTCTGTGACG	600
Qy	601	CACCTTCTATAGTCCACCAAGTATGCGCTCACTGCGCTGACAGAGGAGTCTGAGCAAG	660
Db	601	CACCTTCTATAGTCCACCAAGTATGCGCTCACTGCGCTGACAGAGGAGTCTGAGCAAG	660
Qy	661	CTTGGGAGGCGGAGACCCACATCGGAGCGACGTGCTCTTCCAGGTGTGGTGAGACA	720
Db	661	CTTGGGAGGCGGAGACCCACATCGGAGCGACGTGCTCTTCCAGGTGTGGTGAGACA	720

Qy	721	CAATTGCGCTTCAAACTCCACGACAGGACCCCTGAGAGGAGCTGCCACCTATGAGCAA	780
Db	721	CAATTGCGCTTCAAACTCCACGACAGGACCCCTGAGAGGAGCTGCCACCTATGAGCAA	780
Qy	781	ATGAAGTGTCTCAAAACCGGAGGATGTGGCGAGGCTGTATCTAGCTCCTCAGACACCC	840
Db	781	ATGAAGTGTCTCAAAACCGGAGGATGTGGCGAGGCTGTATCTAGCTCCTCAGACACCC	840
Qy	841	GACACATCCAGATTGGAGACATCCAGATGAGGCCCGGAGGAGTGAATGTGAAATG	900
Db	841	GACACATCCAGATTGGAGACATCCAGATGAGGCCCGGAGGAGTGAATGTGAAATG	900
Qy	901	TGGAGCTCTCCCTCCCTCCGACCCCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG	960
Db	901	TGGAGCTCTCCCTCCCTCCGACCCCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG	960
Qy	961	TGTTGATTTCTGGATCAGGGATACCACTTCTGTCACACCCCGACAGGGGCTAGAAA	1020
Db	961	TGTTGATTTCTGGATCAGGGATACCACTTCTGTCACACCCCGACAGGGGCTAGAAA	1020
Qy	1021	ATTTGTTGAGATTTTATATCATCTTGTCAAATGCTTCAATGTGAAATGTGAAATG	1080
Db	1021	ATTTGTTGAGATTTTATATCATCTTGTCAAATGCTTCAATGTGAAATGTGAAATG	1080
Qy	1081	GGCTGGGGAAGGAGGTGCTCCCTAATGCTTAACTGTTAACTGTTCTGCTGCTGCTG	1140
Db	1081	GGCTGGGGAAGGAGGTGCTCCCTAATGCTTAACTGTTAACTGTTCTGCTGCTGCTG	1140
Qy	1141	TGGGCACTTGGCTTTGCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTGTG	1200
Db	1141	TGGGCACTTGGCTTTGCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTGTG	1200
Qy	1201	GCCAAATCCCACTTCTTGGCACTCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG	1260
Db	1201	GCCAAATCCCACTTCTTGGCACTCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG	1260
Qy	1261	GAGGCTTCACTTATATCTGTTGTTATCCAGGCTCCAGACTTCTCTCTCTCTCTCTG	1320
Db	1261	GAGGCTTCACTTATATCTGTTGTTATCCAGGCTCCAGACTTCTCTCTCTCTCTCTG	1320
Qy	1321	CCCACTGACCTCTCCCTCTTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTG	1380
Db	1321	CCCACTGACCTCTCCCTCTTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTG	1380
Qy	1381	TCCTGCTG	1440
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Qy	1441	GGGCTGGCCAGTGGATTTTCATGTCATTAATAAAGGAAATCGCAACCAAAAAA	1500
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Qy	1501	AAAAA 1505	
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RESULT 12
US-10-174-581-377
; Sequence 377, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RIC41
CURRENT APPLICATION NUMBER: US/10/174,581
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
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PRIOR APPLICATION NUMBER: 60/063121
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PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086023
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086486
PRIOR FILING DATE: 1998-05-22
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PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
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PRIOR APPLICATION NUMBER: 60/087827
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PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05

[illegible]


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; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-749-377

Query Match 100.0%; Score 1505; DB 13; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGGATCGGACCCCAAGCAGGTGCGCGCGCGCGGAGAGAGCGCGCGGCGTCCAGTCC 60
Db 1 CGCGGATCGGACCCCAAGCAGGTGCGCGCGCGCGGAGAGAGCGCGCGGCGTCCAGTCC 60

Qy 61 TCGACCCCGGTGTCGGGCTAGTCCAGCGAGCGCGAGCGCGCGTGGGCCCATGGCCAGG 120
Db 61 TCGACCCCGGTGTCGGGCTAGTCCAGCGAGCGCGAGCGCGCGTGGGCCCATGGCCAGG 120

Qy 121 CCGGGATGAGCGGTGCGCGAGCGCGGTGCGCGTGGTGGGCTCGGGGGGCGATC 180
Db 121 CCGGGATGAGCGGTGCGCGAGCGCGGTGCGCGTGGTGGGCTCGGGGGGCGATC 180

Qy 181 GCGCGCGCGGTGCGCGCGCGCGTGGTCCAGCAGGAGCTGAAGGTGGTGGGCTCGCGCGCG 240
Db 181 GCGCGCGCGGTGCGCGCGCGCGTGGTCCAGCAGGAGCTGAAGGTGGTGGGCTCGCGCGCG 240

Qy 241 ACTGTGGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGTGAAGTGAAGTGAAGTGAAGT 300
Db 241 ACTGTGGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGTGAAGTGAAGTGAAGTGAAGT 300

Qy 301 TTGATCCCGCTACAGATGTGACCTATCAAAATGAAGAGGACATCCCTCTCCATGTTCTCAGCT 360
Db 301 TTGATCCCGCTACAGATGTGACCTATCAAAATGAAGAGGACATCCCTCTCCATGTTCTCAGCT 360

Qy 361 ATCCGTTCTCAGCACAGCGGTGAGACATCGCATCAACAAATGCTGGCTGGCCCGGCGCT 420
Db 361 ATCCGTTCTCAGCACAGCGGTGAGACATCGCATCAACAAATGCTGGCTGGCCCGGCGCT 420

Qy 421 GACACCGTCTCTCAGCAGCAGCAGTGGTGGAGGACATGTTCAATGTGAAGTGAAGTGAAGT 480
Db 421 GACACCGTCTCTCAGCAGCAGCAGTGGTGGAGGACATGTTCAATGTGAAGTGAAGTGAAGT 480

Qy 481 GCCCTCAGCATCTGCACACGGGAGCGCTACAGTCCATGAAGAGCGGAAATGTGGAGAT 540
Db 481 GCCCTCAGCATCTGCACACGGGAGCGCTACAGTCCATGAAGAGCGGAAATGTGGAGAT 540

Qy 541 GGGCAGCATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACC 600
Db 541 GGGCAGCATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACC 600

Qy 601 CACTTCTATAGTCCACCAAGTATGCGGTGCTGCTGCTGAGCAGGAGCTGAGGCAAGAG 660
Db 601 CACTTCTATAGTCCACCAAGTATGCGGTGCTGCTGCTGAGCAGGAGCTGAGGCAAGAG 660
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RESULT 15

US-10-176-914-377

; Sequence 377, Application US/10176914

; Publication No. US20030017543A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

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; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C83
; CURRENT APPLICATION NUMBER: US/10/176,914
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-914-377

Query Match      100.0%; Score 1505; DB 13; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CGCGATCGGACCCCAAGCAGGTGCGCGCGGCGGCGAGAGAGCGCGCGGCTCAGCTCC 60
Db      1  CGCGATCGGACCCCAAGCAGGTGCGCGCGGCGGCGGCGAGAGAGCGCGCGGCTCAGCTCC 60

QY      61  TCGACCCCGGTGTCGGGCTAGTCCAGCGAGGCGGAGCGGCGGCTGAGGCGGCGGCGGCGG 120
Db      61  TCGACCCCGGTGTCGGGCTAGTCCAGCGAGGCGGAGCGGCGGCTGAGGCGGCGGCGGCGG 120

QY      121  CCCGCGATGAGCGGTGCGCGACCGCGCTGGCGCTGGTGACGCGGCGGCGCTCGGGGGGCGATC 180
Db      121  CCCGCGATGAGCGGTGCGCGACCGCGCTGGCGCTGGTGACGCGGCGGCGCTCGGGGGGCGATC 180

QY      181  GCGCGGCGGCTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db      181  GCGCGGCGGCTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240

QY      241  ACTGTGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTGAGGCTACCCGGGACT 300
Db      241  ACTGTGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTGAGGCTACCCGGGACT 300

QY      301  TTGATCCCTCAGATGTGACCTATCAAAATGAAGAGGACATCCTCTCCATGTTCTCAGCT 360
Db      301  TTGATCCCTCAGATGTGACCTATCAAAATGAAGAGGACATCCTCTCCATGTTCTCAGCT 360

QY      361  ATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGTGGCTTGGCGCGGCGCT 420
Db      361  ATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGTGGCTTGGCGCGGCGCT 420

QY      421  GACACCTGTCTCAGGCAGCACAGTGTGTTGGAGGACATGTTCAATGTGAACGTGCTG 480
Db      421  GACACCTGTCTCAGGCAGCACAGTGTGTTGGAGGACATGTTCAATGTGAACGTGCTG 480

QY      481  GCCCTCAGCATCTGCACACGGGAAGCCCTACCAAGTCCATGAAGAGCGGAATGTGACGAT 540
Db      481  GCCCTCAGCATCTGCACACGGGAAGCCCTACCAAGTCCATGAAGAGCGGAATGTGACGAT 540

QY      541  GGGCAGCATTAATCAATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACC 600
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QY      601  CACTTCTATAGTGCACCAAGTATGCGTCACTGGCTGACAGAGGAGTCTGAGGAGAG 660
Db      601  CACTTCTATAGTGCACCAAGTATGCGTCACTGGCTGACAGAGGAGTCTGAGGAGAG 660

QY      661  CTTCCGGAGGCCAGACCCACATCCGAGCCACGTGCACTCTCCAGGTGTGGTGAGACA 720
Db      661  CTTCCGGAGGCCAGACCCACATCCGAGCCACGTGCACTCTCCAGGTGTGGTGAGACA 720

QY      721  CAATTCGCTTCAAACTCCAGCAAGGACCCCTGAGAGGCGAGTGCACCTATGAGCAA 780
Db      721  CAATTCGCTTCAAACTCCAGCAAGGACCCCTGAGAGGCGAGTGCACCTATGAGCAA 780
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Search completed: September 16, 2004, 12:43:53

Job time : 744 secs

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; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
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; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 89
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-89

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Query Match      34.1%; Score 513.6; DB 4; Length 569;
Best Local Similarity 99.4%; Pred. No. 3.3e-123;
Matches 535; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

Qy 968 TTCTGGATCAGGATACCACTTCCTGTCACACCCCGACAGGGCTAGAAAAATTGTT 1027
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Qy 1028 TGAGATTTTATATCATCTTGTCAAAATGCTTCAAGTTGTAAATGTGAAAAATGGCTGG 1087
Db 72 TGAGATTTTATATCATCTTGTCAAAATGCTTCAAGTTGTAAATGTGAAAAATGGCTGG 131

Qy 1088 GAAAGGAGGTGGTCCCTAATTTTACTTGTAACTTCTTGTGCCCCCTGGGCAC 1147
Db 132 GAAAGGAGGTGGTCCCTAATTTTACTTGTAACTTCTTGTGCCCCCTGGGCAC 191

Qy 1148 TTGGCCCTTTGCTCTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGTGTGGCCAAAA 1207
Db 192 TTGGCCCTTTGCTCTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGTGTGGCCAAAA 251

Qy 1208 TCCCATCTTTCTGCACTCAACCTGTGTGCTCAGGGCTGGGTGGGAGGAGGCT 1267
Db 252 TCCCATCTTTCTGCACTCAACCTGTGTGCTCAGGGCTGGGTGGGAGGAGGCT 311

Qy 1268 TCACCTTATATCTGTGTGTATCCAGGCTCCAGACTTCCTCTGCTGCCCTGCCACTG 1327
Db 312 TCACCTTATATCTGTGTGTATCCAGGCTCCAGACTTCCTCTGCTGCCCTGCCACTG 371

Qy 1328 CACCTCTCCCTTATCTATCTCTCTCGGCTCCCGACCCAGCTTGTGCTTCTTGTGTC 1387
Db 372 CACCTCTCCCTTATCTATCTCTCTCGGCTCCCGACCCAGCTTGTGCTTCTTGTGTC 431

Qy 1388 CCCTCTGGGTGTCATCCCTCACTCTGACTGTGATGTGGAGCAGAGAACACAGGCGCTG 1447
Db 432 CCCTCTGGGTGTCATCCCTCACTCTGACTGTGATGTGGAGCAGAGAACACCA-GGCCTG 490

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Qy 1448 GCCCAGTGGATTTTCATGTCATTAATAAAGAAAAATCGACCAAAAAA 1505
Db 491 GCCCAGTGGATTTTCATGTCATTAATAAAGAAAAATCGACCAAAAAA 548

RESULT 2
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; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
; US-08-232-463-14

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Best Local Similarity 3.6%; Pred. No. 2.1e-07;
Matches 12; Conservative 209; Mismatches 117; Indels 0; Gaps 0;

Qy 1082 GCTGGGAAAGAGGTGGTGTCCCTAATTTGTTTACTTGTAACTTGTCTTGTGCCCCCT 1141
Db 1045 GCAGTGCAGGAGCTTGGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1104

Qy 1142 GGGCAGTGGCTTGTCTCTCAGTGTCTTCCCTTTGACATGGGAAAGAGTGTGG 1201
Db 1105 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1164

Qy 1202 CCAAAATCCCATCTTCTTGACCTCAACGCTCTGTGGCTCAGGGCTGGGGTGGCAGAGG 1261
Db 1165 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1224

Qy 1262 AGGCCTTACCTTATCTGTGTGTATCTGTTATCATCAGGGCTCCAGACTTCCTCTCTGCTGCC 1321
Db 1262 AGGCCTTACCTTATCTGTGTGTATCTGTTATCATCAGGGCTCCAGACTTCCTCTCTGCTGCC 1321

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Query Match 3.9%; Score 58.4; DB 4; Length 732;
 Best Local Similarity 46.2%; Pred. No. 1.4e-05;
 Matches 234; Conservative 0; Mismatches 266; Indels 6; Gaps 1;

QY 23 CGGCGCGCGGAGAGAGCGCGCGGTGAGTCTCTCGACCCCGGTGTCGGGCTAGT 82
 Db 524 CAGCCACGCGACGCGAGCGGCGGACTGTCGCTCTCTCCACGCGCTCGCATACACCT 465

QY 83 CCAGCGAGCGGCGCGCGGTGGGCGCATGCGCGGCGCGGTGAGAGCGGTGGCGG 142
 Db 464 ACAAGAACATCAGAGGTGAAGCATGACGCTAGCTGTCGCGAGATTTCTCCCTGTCTT 405

QY 143 ACCGCTGGCGCTGTGACGCGGCGCTCGGCGGCGCATCGGCGCGCGGTGGCGCGCC 202
 Db 404 CCGCGGTGCGCGTGTGACCGCGCGCGGCGCGGCGCATCGGCGGCGCATCGCCCTCGCCC 345

QY 203 TGGTCCAGCAGGAGTGAAGGTGTGGGCTGCGCGCGCATGTGTGGGCAACATCGAGGAGC 262
 Db 344 TGGCGCGCGCGCGCGCGGCGGCGGCGGTGGCGCGGCGCATCGGCGGCGGAGAA 285

QY 263 TGGTGTGCTGAATGAAGAGTGCAGGCTACCGCGGCGCTTTGATCCCTACAGATGTGACC 322
 Db 284 CCGCGCGCGCGCATCGGCGCGCTCGGTGCGCGCGCGGCGGCGGCGGCGGCGGCGG 231

QY 323 TATCAAAATGAAGAGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTG 382
 Db 230 TCAGCGAGCGGCGACAGCGTTCGGCGGATGTTGAGCGGCGGCGGCGGCGGCGGCGG 171

QY 383 TAGACATCTGATCAAAATGCTGGTGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 442
 Db 170 TCGACGTGGCGGTGAACAAATCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 111

QY 443 CCAGTGTGGAAGAGACATGTTCAATGTAAGCGTGTGGCGCGGCGGCGGCGGCGGCGG 502
 Db 110 TCGCGGAGTGGAGCGGCGGTGATGAACGTCACGCGCGCGCGGCGGCGGCGGCGGCGG 51

QY 503 AAGCTACCGTCCATGAAGAGCGG 528
 Db 50 CCGAAGTCCGCTGATCAGCGGCGAG 25

RESULT 7
 US-09-252-991A-15779
 ; Sequence 15779, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 15779
 ; LENGTH: 2073
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-15779

Query Match 3.9%; Score 58.4; DB 4; Length 2073;
 Best Local Similarity 46.2%; Pred. No. 2.2e-05;
 Matches 234; Conservative 0; Mismatches 266; Indels 6; Gaps 1;

QY 23 CGGCGCGCGGAGAGAGCGCGCGGTGAGTCTCTCGACCCCGGTGTCGGGCTAGT 82
 Db 153 CAGCCACGCGACGCGAGGCGGAGTGTGCGCTCTCTCCACGCGCTCGCATACACCT 212

QY 83 CCAGCGAGCGGCGGCGCGGTGGGCGCATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 142

Db 213 ACAAGAACATCAGAGGTGAAGCATGCAAGTACGTGTCGACGATTTCTCCCTGTCTT 272
 QY 143 ACCGCTGGCGCTGTGTAAGCGGCGCGCTCGGCGGCGCATCGGCGCGCGGTGGCGCGGCGCC 202
 Db 273 CCGCGGTGCGCGTGTGATGACCGCGCGGCGGCGGCGCATCGGCGGCGGCGGCGGCGGCGG 332

QY 203 TGGTCCAGCAGGAGTGAAGGTGTGGGCTGCGCGCGCATGTGTGGGCAACATCGAGGAGC 262
 Db 333 TGGCGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 392

QY 263 TGGCTGTGCTGAATGAAGAGTGCAGGCTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 322
 Db 393 CCGCGCGCGGCGATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 446

QY 323 TATCAAAATGAAGAGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTG 382
 Db 447 TCAGCGAGCGGCGACAGCGTTCGGGCGGATGTTGAGCGGCGGCGGCGGCGGCGGCGGCGG 506

QY 383 TAGACATCTGATCAAAATGCTGGCTTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 442
 Db 507 TCGAGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 566

QY 443 CCAGTGTGGAAGAGACATGTTCAATGTAAGCGTGTGGCGCGGCGGCGGCGGCGGCGGCGG 502
 Db 567 TCGCGGAGTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 626

QY 503 AAGCTACCGTCCATGAAGAGCGG 528
 Db 627 CCGAAGTCCGCTGATCAGCGGCGAG 652

RESULT 8
 US-09-252-991A-13796
 ; Sequence 13796, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 13796
 ; LENGTH: 1419
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-13796

Query Match 3.9%; Score 58.2; DB 4; Length 1419;
 Best Local Similarity 49.4%; Pred. No. 2.1e-05;
 Matches 212; Conservative 0; Mismatches 208; Indels 9; Gaps 2;

QY 101 GCGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 160
 Db 702 GGGGATAGCCCATGTCCAAGACCCACCTGTTTCGACCTCGACGCGGCAAGATCGCTTCTT 761

QY 161 CGG 220
 Db 762 CCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 821

QY 221 AGGTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 280
 Db 822 ACCTGATCGTCTCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 881

QY 281 GTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 340
 Db 882 CGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 935

Db 485 TCCTGCTCAACACGCGGGATCATGCTGCTCGGCCGCTGGAGGAGCGCGACACACCG 426
QY 449 GTTGAAGGACATGTTCAATGTGAACGTGCTGCTGCCCTCAGCATCTCCACACGGGAAGCTT 508
Db 425 ACTGGACCCGGATGATCGACACAAATCTCTCTGGGCTGTATGATGATGACACCGCGCGCC 366
QY 509 ACCAGTCCATGAAGGAGCGGAATGTGGAGATGGGCACATCATTAACATCAATAGCATGT 568
Db 365 TTCCCATCTGCTGGCAGCAGGACCGTGGTGAGATGCTCTCGATCGCGGGCGGG 306
QY 569 CTGGCCACCGAGTGTACCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCG 628
Db 305 TGAACGTCCGCAACGCGCGCTCTACAGGCCACGAAATTCGGTGTGAACGGTTCAGCG 246
QY 629 TCACTGCGCTGACAGAGGACTGAGCAGAGCTTCGGGAGGCCACACCCACATCCGAG 688
Db 245 AGACGCTGGCAGAGGTACCGAGCGGGGTGCGGTCTGTCATCGAGCGCGGCA 186
QY 689 CCAGTGTGATCTTCCAGTGTGTGGAGACACAATTCGCTTCAA 734
Db 185 CCACCGACAGGAGTGGCGGCCACATCACCCACCGCCACCA 140

RESULT 11
US-09-726-614-22/c
; Sequence 22, Application US/09726614
; Patent No. 6514735
; GENERAL INFORMATION:
; APPLICANT: Susan E. Jensen
; APPLICANT: Kwamena A Aidoo
; APPLICANT: Ashish S. Paradkar
; TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
; Patent No. 6514735
; TITLE OF INVENTION: Acid Biosynthesis
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN,PPLC
; STREET: The Jennifer Building, 400 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO).
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,614
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/790,462
; FILING DATE: 29-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: D. Douglas Price
; REGISTRATION NUMBER: 24,514
; REFERENCE/DOCKET NUMBER: 1418/P57452US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 39305350
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

Query Match 3.8%; Score 56.8; DB 4; Length 744;
Best Local Similarity 44.9%; Pred. No. 3.7e-05;
US-09-726-614-22

Matches 263; Conservative 0; Mismatches 317; Indels 6; Gaps 1;
QY 149 TGGCGCTGTGATCGGGGGCTCGGGGGCATCGGGGGCGCCCTGGGCCCGGCGCTGTCC 208
Db 719 TGGCGCTCATACGGGGCGAGCTCGGCATCGGGAGGCCACGGCCCGCGCCCTGGCCG 660
QY 209 AGCAGGACTGAAGTGTGGCTGGCCGCACTGTGGGCAACATCGAGGAGCTGGTG 268
Db 659 CCGAGGGCGCCCGCTGGCCATCGCGCGCGCGCGGTGAGAAGCTGCGCGCCCTGGGTG 600
QY 269 CTGAATGTAAGAGTACAGGCTACCCCGGACTTTGATCCCTACAGATGTGACCTATCAA 328
Db 599 AGAAGTGAACCGCCCGGG-----GCGAAGTCCATGTCTCTGAACTCGACGTGCGCG 546
QY 329 ATGAAGAGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACACGCGGTAGACA 388
Db 545 ACCCGACGGGGTGGACCGCGCTCGCTCACCGTCGAGCGCTGGGGCGCTCGACA 486
QY 389 TCTGCATCAACAATGCTGGCTGGCCCGCTGACACCTGCTCTCAGGACGACCAAGTG 448
Db 485 TCCTGCTCAACAACGCGCGGATCATGCTGCTCGGCCCGCTGAGAGCGCGCACACCG 426
QY 449 GTTGAAGGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAGCT 508
Db 425 ACTGACCCGGATGATCGACACCAATCTCTCTGGGCTGATGTACATGACCGGGCGGCC 366
QY 509 ACCAGTCCATGAAGGAGCGGAATGTGACGATGGGCACATCATTAACATCAATAGCATGT 568
Db 365 TTCCCATCTGCTGGCAGCAAGGACCGTGGTGACATGTCCTCGATCGGGCGCGGG 306
QY 569 CTGGCCACCGAGTGTACCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCG 628
Db 305 TGAACGTCCGCAACGCGCGCTTACAGGCCACGAAATTCGGTGTGAACGGTTCAGCG 246
QY 629 TCACTGCGCTGACAGAGGACTGAGGCAAGAGCTTCGGGAGGCCACACCCACATCCGAG 688
Db 245 AGACGCTGGCAGAGGTACCGAGCGGGGTGCGGTCTGTCATCGAGCGCGGCA 186
QY 689 CCAGTGTGATCTTCCAGTGTGTGGAGACACAATTCGCTTCAA 734
Db 185 CCACCGACAGGAGTGGCGGCCACATCACCCACCGCCACCA 140

RESULT 12
US-09-385-040-22/c
; Sequence 22, Application US/09385040
; Patent No. 6589775
; GENERAL INFORMATION:
; APPLICANT: Jensen, Susan E
; APPLICANT: Aidoo, Kwamena A
; APPLICANT: Paradkar, Ashish S
; TITLE OF INVENTION: DNA SEQUENCE ENCODING ENZYMES OF CLAVULANIC ACID
; TITLE OF INVENTION: BIOSYNTHESIS
; FILE REFERENCE: 09/385,040
; CURRENT APPLICATION NUMBER: US/09/385,040
; PRIOR FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 08/790,462
; PRIOR FILING DATE: 1997-01-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Streptomyces clavuligerus
US-09-385-040-22

Query Match 3.8%; Score 56.8; DB 4; Length 744;
Best Local Similarity 44.9%; Pred. No. 3.7e-05;
Matches 263; Conservative 0; Mismatches 317; Indels 6; Gaps 1;
QY 149 TGGCGCTGTGATCGGGGGCTCGGGGGCATCGGGGGCGCTGGGCCCGGCGCTGTCC 208
Db 719 TGGCGCTCATACGGGGCGAGCTCGGCATCGGGAGGCCACGGCCCGCGCCCTGGCCG 660

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QY 209 AGCAGGACTGAAGTGTGGTGGTGGCCCGCCCACTGTGGGCAACATCAGAGAGTGGGTG 268
Db      |||||
QY 659 CCGAGGGCGCGCGTGGCCATCGCCGCGCGCGGTCGAGAAGTGGCGCCCTGGGTG 600
Db      |||||
QY 269 CTGAATGAAGTGCAGGCTACCCGGACTTTTGTATCCCTACAGATGTGACATCAA 328
Db      |||||
QY 599 ACAGAGTGAACCGCGCGCGG-----GGAAGGTCCATGTCTCGAACTCGACGTGGCG 546
Db      |||||
QY 329 ATGAAGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACA 388
Db      |||||
QY 545 ACCGGCAGGGGTGGACGCGCGCGTGGCTCCACGTCGAGGCGTGGCGGCGCTCGACA 486
Db      |||||
QY 389 TCTGCATCAACAATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 448
Db      |||||
QY 485 TCCTCGTCAACAACGCGCGGATCATGTCTCGCGCGCGTGGAGGACCGCCGACACCG 426
Db      |||||
QY 449 GTTCGAGGACATGTTCAATGTGAACGTGCTGGCGCTCAGCATCTGCACACGGAAGCCT 508
Db      |||||
QY 425 ACTGGACCGGATGATCGACACCAATCTCTGGGCTGTATGATGATGATGATGATGATG 366
Db      |||||
QY 509 ACCAGTCCATGAAGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATGT 568
Db      |||||
QY 365 TTCCCATCTGCTGGCAGCAAGGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 306
Db      |||||
QY 569 CTGGCCACCGAGTGTACCCCTGTCTGTGACCACTTCTATAGTCCACCAAGTATGCGG 628
Db      |||||
QY 305 TGAACGTCCGCAACCGCGCGCTCTACCAAGGCCACGAAGTTCGGTGTGAACGCTTCAGCG 246
Db      |||||
QY 629 TCACGTGCTGACAGAGGACTGAGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAG 688
Db      |||||
QY 245 AGACCTGCGCAGGAGTCCAGGAGCGCGGGTCCGGTGTGATGATGATGATGATGATGATG 186
Db      |||||
QY 689 CCACGTGATCTCTCAGGTGTGTGGAGACACAATTCGCTTCAA 734
Db      |||||
QY 185 CCACCGACAGGAGTGGCGGCGCCACATCACCACACCGCCACCAA 140
Db      |||||

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RESULT 13

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US-09-385-028-13/c
; Sequence 13, Application US/09385028
; Patent No. 6232106
; GENERAL INFORMATION:
; APPLICANT: Susan E. Jensen
; APPLICANT: Kwamena A Aidoo
; APPLICANT: Ashish S. Paradkar
; TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
; Patent No. 6232106
; TITLE OF INVENTION: Acid Biosynthesis
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: JACOBSON, PRICE, HOLMAN & STERN, PLLC
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004

```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452US2

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TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 39305350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11604 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-385-028-13

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Query Match 3.8%; Score 56.8; DB 3; Length 11604;

Best Local Similarity 44.9%; Pred. No. 0.00012; Matches 263; Conservative 0; Mismatches 317; Indels 6; Gaps 1;

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QY 149 TGGCGCTGGTACCGGGGCGCTCGGGGGGCGATCGGGGGCGGTGGCGCGGCGCTGGTCC 208
Db      |||||
QY 11308 TCGCGCTCATCACGGGCGGAGCTCGGGCATCGGGAGGCCACGGCGCGCCCTGGCGG 11249
Db      |||||
QY 209 AGCAGGAGTGAAGTGTGGGCTGGCGCCGCACTGTGGGCAACATCGAGAGCTGGGTG 268
Db      |||||
QY 11248 CCGAGGGCGCGCGCTGGCCATCGCGCGCGCGGTGCGAAGCTGCGCGCCCTGGGTG 11189
Db      |||||
QY 269 CTGAATGTAAGAGTGCAGGCTACCCCGGACTTTGATCCCTACAGATGTGACCTATCAA 328
Db      |||||
QY 11188 ACGAGTGAACCGCGCGCGG-----GGAAGGTCCATGTCTCGAACTCGACGTGGCG 11135
Db      |||||
QY 329 ATGAAGAGGACATCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACA 388
Db      |||||
QY 11134 ACCGCGAGGGGTGGAGCGCGCGCTCGCTCCACGTCGAGGCGTGGCGCGCTCGACA 11075
Db      |||||
QY 389 TCTGCATCAACAATGCTGGCTGGCGCGCGCTGACACCTGCTCTCAGGAGCAGCAGTG 448
Db      |||||
QY 11074 TCCTCGTCAACACACCGCGGATCATGTCTGCGCGCGGTGGAGAGCGCCGACACCG 11015
Db      |||||
QY 449 GTTGAAGGACATGTTCAATGTGAACGTGCTGGCGCTCAGCATCTGCACACGGAAGCCT 508
Db      |||||
QY 11014 ACTGACCGGATGATCGACCAATCTCTGGGCTGTGTATCATGACCGGGCGGCC 10955
Db      |||||
QY 509 ACCAGTCCATGAAGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGATGT 568
Db      |||||
QY 10954 TTCCCATCTGCTGGCAGCAAGGACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 10895
Db      |||||
QY 569 CTGGCCACCGAGTGTACCCCTGTCTGTGACCCACTTCTATAGTCCACCAAGTATGCGG 628
Db      |||||
QY 10894 TGAACGTCCGCAACCGCGCGCTCTACCGGCGCGAAGTTCGGTGTGAACGCTTCAGCG 10835
Db      |||||
QY 629 TCACGTGCTGACAGAGGAGTGAAGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAG 688
Db      |||||
QY 10834 AGACGCTGGCCAGAGGTCAACGAGCGCGGGTGGGTGGTGGTGGTGGTGGTGGTGG 10775
Db      |||||
QY 689 CCACGTGATCTCTCAGGTGTGTGGAGACACAATTCGCTTCAA 734
Db      |||||
QY 10774 CCACCGACAGGAGTGGCGGCGCCACATCACCACACCGCCACCAA 10729
Db      |||||

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RESULT 14

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US-09-726-614-13/c
; Sequence 13, Application US/09726614
; Patent No. 6514735
; GENERAL INFORMATION:
; APPLICANT: Susan E. Jensen
; APPLICANT: Kwamena A Aidoo
; APPLICANT: Ashish S. Paradkar
; TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
; Patent No. 6514735
; TITLE OF INVENTION: Acid Biosynthesis
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: JACOBSON, PRICE, HOLMAN & STERN, PLLC
; STREET: The Jennifer Building, 400 Seventh Street, N.W.

```

/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/726,614
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/790,462
/ FILING DATE: 29-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: D. Douglas Price
/ REGISTRATION NUMBER: 24,514
/ REFERENCE/DOCKET NUMBER: 1418/P57452US2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 638-6666
/ TELEFAX: (202) 39205350
/ TELEX: RCA 248593 IDEA UR
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11604 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-09-726-614-13

Query Match 3.8%; Score 56.8; DB 4; Length 11604;
Best Local Similarity 44.9%; Pred. No. 0.00012;
Matches 263; Conservative 0; Mismatches 317; Indels 6; Gaps 1;

QY 149 TGGCGCTGTGACGGGGGCGCTCGGGGGGCATCGGGGGCGTGGCCGGCGCCCTGGTCC 208
Db 11308 TCGCGCTCATCAGGGCGGAGCTCGGGCATCGGGAGGCCACGGCCCGCCCTGGCGG 11249

QY 209 AGCAGGACTGAAGTGTGGGTGCGCCCGACCTGTGGGCAACATCGAGGAGTGGGTG 268
Db 11248 CCGAGGGCGCGCGTGCCTATCGCCGCGCGCGGTGAGAACTGCGCCCTGGGTG 11189

QY 269 CTGAATGTAAAGTGTGAGGCTACCCCGGACTTTGATCCCTACAGATGTACCTATCAA 328
Db 11188 ACGAGCTGACCGCCCGCGG-----GCGAAGGTCCATGTCTCGAACTCGACGTCGCGG 11135

QY 329 ATGAAGAGGACATCTCTCCATGTCTCAGTATCCGTTCTCAGCACAGCGGTGTAGACA 388
Db 11134 ACCGGCAGGGGTGAGCGCCCGCTCGCTCCAGCTCGAGGCGCTGGGGCGGCTCGACA 11075

QY 389 TCTGCATCAACAATGTGGTGTGGCCCGGCTGACACCCCTGCTCTCAGGACGACCAAGT 448
Db 11074 TCCTCGTCAACAACGCGGGATCATGTCTCGCCCGGTGGAGGAGCGCGACACCG 11015

QY 449 GTTGAAGGACATGTTCAATGTGAAGTGTGAGCGCTGGCCCTCAGCATCTGACAGGGAAGCT 508
Db 11014 ACTGGACCGGATGATCGACACCAATCTCTGGGCGCTGATGTATACCGCGGCGGCC 10955

QY 509 ACCAGTCCATGAAGGAGCGGAATGTGGACGATGGGCACATCAATTAACATCAATAGCATGT 568
Db 10954 TTCCCATCTGCTGGCAGCAAGGACCGCTGTGTGAGATGTCTCGATCGGGCGCGG 10895

QY 569 CTGGCCACCGAGTGTACCCCTGTGTGTGACCACTTCTATAGTGGCCACCAAGTATCCCG 628
Db 10894 TGAACGTCCGCAACGCGCGCTCTACAGGCGCAGAACTTCGGTGTGAACGCGTTCAGCG 10835

QY 629 TCAGTGGCTGACAGAGGACTAGGCAAGAGCTTCGGGAGGCGCCAGACCAATCCGAG 688
Db 10834 AGACGTGCGCCAGGAGGTACCGAGCGGGGTGCGGGTCTGTCATCGAGCCGGGCA 10775

QY 689 CCACGTGCATCTCTCCAGTGTGGTGGAGACACAATTCGCTTCAA 734
Db 10774 CCACGACACGGAGCTCGCGGCCACATCACCCACACCGCCACCAA 10729

RESULT 15
US-09-385-040-13/c
/ Sequence 13, Application US/09385040
/ Patent No. 6589775
/ GENERAL INFORMATION:
/ APPLICANT: Jensen, Susan E
/ APPLICANT: Aideo, Kwanena A
/ APPLICANT: Paradkar, Ashish S
/ TITLE OF INVENTION: DNA SEQUENCE ENCODING ENZYMES OF CLAVULANIC ACID
/ FILE REFERENCE: 09/385,040
/ CURRENT APPLICATION NUMBER: US/09/385,040
/ CURRENT FILING DATE: 1999-08-30
/ PRIOR APPLICATION NUMBER: US 08/790,462
/ PRIOR FILING DATE: 1997-01-29
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 13
/ LENGTH: 11604
/ TYPE: DNA
/ ORGANISM: Streptomyces clavuligerus
/ US-09-385-040-13

Query Match 3.8%; Score 56.8; DB 4; Length 11604;
Best Local Similarity 44.9%; Pred. No. 0.00012;
Matches 263; Conservative 0; Mismatches 317; Indels 6; Gaps 1;

QY 149 TGGCGCTGTGACGGGGGCGCTCGGGGGGCATCGGGGGCGTGGCCGGCGCCCTGGTCC 208
Db 11308 TCGCGCTCATCAGGGCGGAGCTCGGGCATCGGGAGGCCACGGCCCGCCCTGGCGG 11249

QY 209 AGCAGGACTGAAGTGTGGGTGCGCCCGACCTGTGGGCAACATCGAGGAGTGGGTG 268
Db 11248 CCGAGGGCGCGCGTGCCTATCGCCGCGCGCGGTGAGAACTGCGCCCTGGGTG 11189

QY 269 CTGAATGTAAAGTGTGAGGCTACCCCGGACTTTGATCCCTACAGATGTACCTATCAA 328
Db 11188 ACGAGCTGACCGCCCGCGG-----GCGAAGGTCCATGTCTCGAACTCGACGTCGCGG 11135

QY 329 ATGAAGAGGACATCTCTCCATGTCTCAGTATCCGTTCTCAGCACAGCGGTGTAGACA 388
Db 11134 ACCGGCAGGGGTGAGCGCCCGCTCGCTCCAGCTCGAGGCGCTGGGGCGGCTCGACA 11075

QY 389 TCTGCATCAACAATGTGGTGTGGCCCGGCTGACACCCCTGCTCTCAGGACGACCAAGT 448
Db 11074 TCCTCGTCAACAACGCGGGATCATGTCTCGCCCGGTGGAGGAGCGCGACACCG 11015

QY 449 GTTGAAGGACATGTTCAATGTGAAGTGTGAGCGCTGGCCCTCAGCATCTGACAGGGAAGCT 508
Db 11014 ACTGGACCGGATGATCGACACCAATCTCTGGGCGCTGATGTATACCGCGGCGGCC 10955

QY 509 ACCAGTCCATGAAGGAGCGGAATGTGGACGATGGGCACATCAATTAACATCAATAGCATGT 568
Db 10954 TTCCCATCTGCTGGCAGCAAGGACCGCTGTGTGAGATGTCTCGATCGGGCGCGG 10895

QY 569 CTGGCCACCGAGTGTACCCCTGTGTGTGACCACTTCTATAGTGGCCACCAAGTATCCCG 628
Db 10894 TGAACGTCCGCAACGCGCGCTCTACAGGCGCAGAACTTCGGTGTGAACGCGTTCAGCG 10835

QY 629 TCAGTGGCTGACAGAGGACTAGGCAAGAGCTTCGGGAGGCGCCAGACCAATCCGAG 688
Db 10834 AGACGTGCGCCAGGAGGTACCGAGCGGGGTGCGGGTCTGTCATCGAGCCGGGCA 10775

QY 689 CCACGTGCATCTCTCCAGTGTGGTGGAGACACAATTCGCTTCAA 734
Db 10774 CCACGACACGGAGCTCGCGGCCACATCACCCACACCGCCACCAA 10729

Search completed: September 16, 2004, 12:21:20
Job time : 150 secs

A handwritten mark, possibly a signature or initials, is written over a horizontal line. The mark consists of a large, stylized 'J' or 'G' shape with a small crossbar.